(A) LENGTH: 286 base pairs (B) TYPE: nucleic acid

5	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:	
10	AGTGCCAGTG ATTAACTGCA TTTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA	60
	AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT	120
	CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACANTGCNAG	180
15	TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG	240
	TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC	286
20	(2) INFORMATION FOR SEQ ID NO: 4602:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 264 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:	
30	ATATGGCTAT GGTATTCACA TATCGATNAA CATGGACATA ACTCATGCTG GGTTTCCCCA	60
	TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT	120
25	AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA	180
35	TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG	240
	nTTAAACGGG GTATTAATCT TGTG	264
40	(2) INFORMATION FOR SEQ ID NO: 4603:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 246 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:	
50	GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC	60
	GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA	120
55	ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT	180

	TATCCn	246
5	(2) INFORMATION FOR SEQ ID NO: 4604:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 248 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:	
15	ATTAACTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT	60
	Ancgccatgc tggctcgttt ttcaaatcaa gccattttaa attitggaaa ggtgtatgga	120
00	CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA	180
20	GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn	240
	TTTGATGG	248
25	(2) INFORMATION FOR SEQ ID NO: 4605:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 246 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:	
35	CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT	60
	AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT	120
40	ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT	180
70	GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn	240
	TGGGTT	246
45	(2) INFORMATION FOR SEQ ID NO: 4606:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs	
50	<ul><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:	

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	TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG	120
	ATGTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC	180
5	TGCAGTTATT TCAGTTTCTG CTTCACGCTn CT	212
	(2) INFORMATION FOR SEQ ID NO: 4607:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 266 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:	
	TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT	60
20	GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA	120
	ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT	180
	AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC	240
25	GGAATCGAAG CCCCAGTAAA CGGCGG	266
	(2) INFORMATION FOR SEQ ID NO: 4608:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 215 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:	
	TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTANATTA AAGCAGTTTC TGGATCTGGT	60
40	AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA	120
	GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA	180
	CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG	215
45	(2) INFORMATION FOR SEQ ID NO: 4609:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 241 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	GGGTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG	60
5	CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG	120
	GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT	180
	TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATNGATTAGC	240
10	С	241
	(2) INFORMATION FOR SEQ ID NO: 4610:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 215 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:	
	ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG	60
25	CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC	120
25	TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG	180
	TTTCAnTTCG CCAAGCCATT TTTCTTTGGT GnTTA	215
30	(2) INFORMATION FOR SEQ ID NO: 4611:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 400 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:	
40	GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA	60
	TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTTGATA AATATGGCGT GCGTTTGGCA	120
45	ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA	180
	TGCAGTACCG TGTTTGTTGA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT	240
	TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC	300
50	TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG	360
	GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA	400
	(2) INFORMATION FOR SEQ ID NO: 4612:	
55		

(A) LENGTH: 258 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:	
10	AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA	60
	TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC	120
	TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC	180
15	CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG	240
	ACCGTTAAGG TTnAAAGG	258
20	(2) INFORMATION FOR SEQ ID NO: 4613:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 210 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:	
30	GACTTCGTTT CAGTGTAAAA TTTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG	60
	ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC	120
	TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC	180
35	AGCTTTTTC TACAGCTTTT ACAATATTnn	210
	(2) INFORMATION FOR SEQ ID NO: 4614:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 235 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:	
	TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG	60
50	AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGNATCGCT	120
	ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA	180
5.5	GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA	235
55		

(i) SEQUENCE CHARACTERISTICS:

5	<ul><li>(A) LENGTH: 209 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:	
	ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAANTTTA	60
	TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTCG ATGCTTTAAT TCAGTTAGAA	120
15	GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG	180
	TCnTTGGATA GAGTTACAAA CTTATTTTG	209
	(2) INFORMATION FOR SEQ ID NO: 4616:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 222 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:	
30	ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA	60
	TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT	120
	GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC	180
35	CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT	222
	(2) INFORMATION FOR SEQ ID NO: 4617:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 258 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:	
	CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCATTTC TGCGATTTCT	60
50	TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA	120
	ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGNGATC TCTTGTAATG	180
55	TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT	240

	(2) INFORMATION FOR SEQ ID NO: 4618:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 216 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:	
	TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAn	60
15	CAGTAAGATA ATTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT	120
	CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT	180
	GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT	216
20	(2) INFORMATION FOR SEQ ID NO: 4619:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 238 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:	
	ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA	60
	GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT	120
35	GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA	180
	TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG	238
	(2) INFORMATION FOR SEQ ID NO: 4620:	
40 45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 249 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:	
50	AACCATTGAA GCACCCCATT ACGTTTTGGC TGACACGNAC GTATATCGCC TGCCCAAGCA	60
	GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC	120
	CATTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG	180

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	TIGACCAGC	249
	(2) INFORMATION FOR SEQ ID NO: 4621:	
5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 267 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:	
15	TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG	60
	TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG	120
	TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA	180
20	AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC	240
	ACAGTCTCGG GCGATTGTCG AGTCCAC	267
25	(2) INFORMATION FOR SEQ ID NO: 4622:	
23	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 231 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
30	(D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:	
35	CAAAAGGTAG TTTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT	60
	TAAAAGGAng ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA	120
	TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC	180
40	GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C	231
	(2) INFORMATION FOR SEQ ID NO: 4623:	231
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 301 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:	
	CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA	60
EE		

	CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA	180
	CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA	240
5	AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA	300
	A	301
10	(2) INFORMATION FOR SEQ ID NO: 4624:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 222 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:	
20	CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA	60
	GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA	120
25	GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT	180
25	TTTGAAAAAG GGGNAAATCA TAATCATTNG GCGATGCCCA AG	222
	(2) INFORMATION FOR SEQ ID NO: 4625:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 301 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:	
	TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC	60
40	CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT	120
	AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC	180
45	CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTANGTT	240
	CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA	300
	A	301
50	(2) INFORMATION FOR SEQ ID NO: 4626:	
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 223 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:	
5	GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG	60
	CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA	120
10	CATTAATCCC ATTTTTANCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG	180
	TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC NAT	223
	(2) INFORMATION FOR SEQ ID NO: 4627:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 221 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:	
25	TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG	60
25	GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC	120
	TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT	180
30	AAAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T	221
	(2) INFORMATION FOR SEQ ID NO: 4628:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 208 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:	
	ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGNATTA TATAACACGA GGTGTAGTAA	60
45	GTATGAAATT TGAGNAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC	120
	GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTTAAATCTG TATGTGTGAA	180
	TCCACCACAT GTTAAATATG CAGCAGAG	208
50	(2) INFORMATION FOR SEQ ID NO: 4629:	
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 305 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
J 5		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:	
	ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG	60
5	TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC	120
	ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA	180
10	ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA	240
	TTGATACTNT ATCGAGAGCG TGAGNGAACT GAATACTGCG CTCACGGTAT TACATGCGTG	300
	CACTG	305
15	(2) INFORMATION FOR SEQ ID NO: 4630:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 213 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:	
	TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGTGTGACT	60
	CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAAACTAG ATAGTAAGTA	120
30	AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT	180
	CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA	213
	(2) INFORMATION FOR SEQ ID NO: 4631:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 213 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:	
45	GARGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA	60
	TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA	120
	ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG	180
50	GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA	213
	(2) INFORMATION FOR SEQ ID NO: 4632:	

5	<ul><li>(A) LENGTH: 205 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:	
10	GCTTTTAAAT CAAATGATAG CGGAAGGGNA TTTTAAAATT ATTCGAACCA TTATTTACAG	60
	CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG	120
	TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA	180
15	TCGAAGCGAA CTTCAAGTTG CTTCA	205
	(2) INFORMATION FOR SEQ ID NO: 4633:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 204 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:	
	AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA	60
30	CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnT ACTTTTTCTn TAGAAATTAG	120
	TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG	180
	CTAATGTGTT AAGAACTACT ACAT	204
35	(2) INFORMATION FOR SEQ ID NO: 4634:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 226 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:	
	GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG	60
	AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGCGTTACGT TAGCCCGTCT GATGTAGAAG	120
50	CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG	180
	AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA	226
55	(2) INFORMATION FOR SEQ ID NO: 4635:	

5	<ul><li>(A) LENGTH: 208 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:	
10	CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC	60
	GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG	120
	AAATAGGTCA TAGGATANAA CNGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG	180
15	GCTTAAGTTG GCCATTTTTC ATATGGTC	208
	(2) INFORMATION FOR SEQ ID NO: 4636:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 228 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:	
	TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAA GTAGACCTTG	60
30	CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA	120
	CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC	180
25	TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG	228
<i>35</i>	(2) INFORMATION FOR SEQ ID NO: 4637:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 212 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:	
	CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACTTATA GATGGATCCG CGCTGCATTA	60
	GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA	120
50	TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGNATC	180
	TTCCGCAATT GGCGAAAGCT GTACGGGCAA CG	212
55	(2) INFORMATION FOR SEQ ID NO: 4638:	

(A) LENGTH: 256 base pairs(B) TYPE: nucleic acid

5	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:	
10	ATRITRATTAA ATAGAGAACA GCAGTAAGAT ATTITCTAAT TGAAAATTAT CTTACTGCTG	60
	TITTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTTAAATTTC GATAATTTTT	120
	CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT	180
15	TACATTTCCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA	240
	GGTTAGGATA AAGAGG	256
20	(2) INFORMATION FOR SEQ ID NO: 4639:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 209 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:	
50	ANAGNAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT	60
	GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT	120
35	GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA  AATCTAACCA TCTATTAAAT TTTAAAACC	180
	(2) INFORMATION FOR SEQ ID NO: 4640:	209
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:	
50	ngnaaaggtg aaaagcaccc cggaagggag gtgaaataga acctgaaacc gtgtgcttac	60
	AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT	120
	ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG	180
55	GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT	224

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:	
	CACTCACnCA GATTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	60
	AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC	120
15	CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTANG	180
	ATCCTAAGTC TAGTGCGTCT GCCAA	205
	(2) INFORMATION FOR SEQ ID NO: 4642:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 235 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:	
30	AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC	60
	CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA	120
	GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT	180
35	ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG	235
	(2) INFORMATION FOR SEQ ID NO: 4643:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 260 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:	
	AGNAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA	60
50	CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA	120
	GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC	180
	ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC	240
55		

	(2) INFORMATION FOR SEQ ID NO: 4644:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 285 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:	
	CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG	60
15	TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA	120
	ATTTATTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCCCTT	180
	GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG	240
20	TTCAGTCCAC TACTGGCAAT ATAACTTGTA GAGCTAGGAC ATTGG	285
	(2) INFORMATION FOR SEQ ID NO: 4645:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 206 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:	
	GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG	60
35	CGCTTGTnTG GGGGTTCAAC TGGAAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn	120
	TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG	180
	ATTTAGATGG TGGCTTTTGA TAAACA	206
40	(2) INFORMATION FOR SEQ ID NO: 4646:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 222 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:	
	ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA	60
	CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA	120

	Cngacagtga ttcagattca gacagcgact cagattcnga ta	222
	(2) INFORMATION FOR SEQ ID NO: 4647:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 200 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:	
15	GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTTGCTT AATGAATGCT TTTTCTTCGT	60
	TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA	120
	GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA	180
20	CCGAAATTAA TGACAGTCCA	200
	(2) INFORMATION FOR SEQ ID NO: 4648:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 201 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:	
	CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC	60
35	ACGCAGGANG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAACT	120
	AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATANA GAGTTTTAAA	180
	TAAGCTTGGA ATTCATTAAG A	201
40	(2) INFORMATION FOR SEQ ID NO: 4649:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 218 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:	
	AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA	60
	ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG	120
55		

	AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTNAAAT	218
	(2) INFORMATION FOR SEQ ID NO: 4650:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 202 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:	
15	GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT	60
	AGAAGTAAAA GCCATCAGGT GGCGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG	120
	CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG	180
20	ATTCnGATTA CTAATATnTA TG	202
	(2) INFORMATION FOR SEQ ID NO: 4651:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 209 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:	
	AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGNA TAACTTCNGG	60
35	AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC	120
	TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC	180
	CAAGGCAACG ATGCATAGCC GACCTGAGA	209
40	(2) INFORMATION FOR SEQ ID NO: 4652:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 202 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:	
	TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG	60
	ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT	120
55		

	CCACTTATCG TGGTTGGAGA CA	202
	(2) INFORMATION FOR SEQ ID NO: 4653:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 205 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:	
15	CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA	60
	TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT	120
	ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG	180
20	AACCGGTACG TGATCACTCA ACnGn	205
	(2) INFORMATION FOR SEQ ID NO: 4654:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 264 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:	
	AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC	60
35	ATTAACTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT	120
	GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT	180
	AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn	240
40	CTATTAATCC ACACGGGTTA GANG	264
	(2) INFORMATION FOR SEQ ID NO: 4655:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 211 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:	
	GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG	60
55		

	AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG	180
	AAATCAGTTT GCTCTTGGCT GCAGTAAATC G	211
5	(2) INFORMATION FOR SEQ ID NO: 4656:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 212 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:	
	TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT	60
	GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAAGA GACCTTGCGG TCTCAATGCG	120
20	GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT	180
	ACCATCGACG CTAAGGNGCT TAACTGNTGG GT	212
	(2) INFORMATION FOR SEQ ID NO: 4657:	
25 30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 200 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:	
35	TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC	60
	AGCTGGGNAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC	120
	CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC	180
40	CGAGTGAATA AAGAGTTTTA	200
	(2) INFORMATION FOR SEQ ID NO: 4658:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 185 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:	
	TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT	60
55		

	CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG	180
	AAAAn	185
5	(2) INFORMATION FOR SEQ ID NO: 4659:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:	
	AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAGC ACTCCGCCTG	60
	GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA	120
20	GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC	180
	AACTCTAGAG ATAGAGCCTT CCCCTTCG	208
25	(2) INFORMATION FOR SEQ ID NO: 4660:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 365 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:	
35	ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTTAAAGTCA	60
	CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA	120
	GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT	180
40	GATAGAAATC ACTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT	240
	ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC	300
45	GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT	360
	CTGTC	365
	(2) INFORMATION FOR SEQ ID NO: 4661:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 209 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:	
	AAAGTATTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT	60
5	CCAATTCTCC THATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT	120
	CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTCT	180
10	ACATGAAATT TTTCCAAGTG ATATATTTT	209
	(2) INFORMATION FOR SEQ ID NO: 4662:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 246 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:	
	TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA	60
	AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC	120
25	CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA	180
	CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG	240
30	GCCTAA	246
	(2) INFORMATION FOR SEQ ID NO: 4663:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 226 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:	
	AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT	60
45	TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG	120
,0	CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA	180
	AAGCAGGCGT AGATTATCAA AGNTTTTGGT ATGCAACCAG CACACT	226
50	(2) INFORMATION FOR SEQ ID NO: 4664:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:	
5	TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT	60
	CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA	120
	GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC	180
10	CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC	234
	(2) INFORMATION FOR SEQ ID NO: 4665:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 196 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:	
	GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT	60
25	CTAAACGTTT AATTMACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACT CATCGCGTAC	120
	AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC	180
30	CATTTTTGCA CGAATT	196
30	(2) INFORMATION FOR SEQ ID NO: 4666:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 226 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:	
	CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT	60
	TAGATTGTGG TTTTTTAGTT GGTGCCATGC TTTAACCTTT TCATTGATTT CAATAACAGG	120
45	TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn	180
	GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTTG GATTTC	226
50	(2) INFORMATION FOR SEQ ID NO: 4667:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 187 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
<i>55</i>		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:	
5	GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGANAA CCGGTGATCT ACCCTTGGTC	60
	AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA	120
10	GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC	180
	CGAAATA	187
	(2) INFORMATION FOR SEQ ID NO: 4668:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 182 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:	
25	CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT	60
	GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA	120
	TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn	180
30	TT	182
	(2) INFORMATION FOR SEQ ID NO: 4669:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 182 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:	
	AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGALAATGG	60
45	TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC	120
	AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT	180
	TT	182
50	(2) INFORMATION FOR SEQ ID NO: 4670:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 185 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
55	(C) SIGNOEDHESS. COUDIE	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:	
5	GGGGCAAAGT CATTECATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG	60
	CACCTTTAA AGTATTACGT AATGTTGTGT TGCGTTTACA TCTTACCCAA AGTGCTAATG	120
10	CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG	180
10	ATTGG	185
	(2) INFORMATION FOR SEQ ID NO: 4671:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 200 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:	
0.5	CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA	60
25	GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA	120
	GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG	180
30	CATTGAGACC GCAAGGnTnT	200
	(2) INFORMATION FOR SEQ ID NO: 4672:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:	
	CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC	60
45	ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTCGC CATTAAAGCG nACGnTGCTG	120
	GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC	180
	TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCG TGCCACGCAT	240
50	AGTGGGTAGT ATGTGTGGAC G	261
	(2) INFORMATION FOR SEQ ID NO: 4673:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 184 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:	
	ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG	60
10	AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA	120
10	ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG	
	CGTT	180
15	(2) INFORMATION FOR SEQ ID NO: 4674:	184
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 203 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:	
	CCCAGTCAAA CTGCCCGCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA	60
	GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT	120
30	CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA	180
	AAGCTCCACG GGGTTCTTTC CGT	203
	(2) INFORMATION FOR SEQ ID NO: 4675:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 229 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(b) TOPOLOGI: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:	
45	nngtttgtaa ataatatggt ggagactagc gggatcgaac cgctgacctc ctgcgtgcaa	60
	AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA	120
	GGATTCGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC	180
50	TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTAA	229
	(2) INFORMATION FOR SEQ ID NO: 4676:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs	

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:	
		60
	TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTCA	60
10	TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC	120
	TTACAAATTT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT	178
	(2) INFORMATION FOR SEQ ID NO: 4677:	
15 20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 286 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:	
25	GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG	60
	TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA	120
	TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA	180
30	AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA	240
	GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAAn	286
	(2) INFORMATION FOR SEQ ID NO: 4678:	
<i>35</i> <i>40</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 229 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:	
45	CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTTA	60
	CACCTATACC TCGTTCCGGA AGGANTGTTC TAAAAGTGAA CTACTCCCGC AATATTAAAT	120
	ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA	180
50	AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACn	229
	(2) INFORMATION FOR SEQ ID NO: 4679:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 173 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(wi) CHOMINGE PROGRESSION OF THE WAR	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:	
	ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT	60
10	CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG	120
	ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC	173
	(2) INFORMATION FOR SEQ ID NO: 4680:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 183 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:	
25	AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA	60
	TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT	120
	AATGNATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT	180
30	ccc	183
	(2) INFORMATION FOR SEQ ID NO: 4681:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 203 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:	
	CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG	60
45	AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTTCCG TCGTACTCAG GATCCACTCA	120
	AGAGAGACAA CATTTTCGAC TACAGGATTA NTACCTTCTT TGATTCATCT TTCCAGATGA	180
	TTCGTCTAAT GTCGTCCTTT GTA	203
50	(2) INFORMATION FOR SEQ ID NO: 4682:	
55	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 187 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:	
	GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT	60
5	CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC	120
	GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC	180
10	ACAAAGA	187
10	(2) INFORMATION FOR SEQ ID NO: 4683:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 187 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:	
	GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG	60
	TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG	120
25	CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT	180
	TTAAATT	187
30	(2) INFORMATION FOR SEQ ID NO: 4684:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 168 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:	
40	AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA	60
	AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA	120
45	AGCTTATTTA AAACTCTTTA TTCACTCGGT TTTGTAAAAT CTATATTT	168
	(2) INFORMATION FOR SEQ ID NO: 4685:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 168 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:	
_	ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA	60
5	ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG	120
	AGCGCCTGCT TThCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT	168
10	(2) INFORMATION FOR SEQ ID NO: 4686:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 174 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:	
20	ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT	60
	TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT CGCATACTGC	120
25	nttattttca aaaaatcaaa tgctcatita caaaagtaaa ctccgcttt aatt	174
25	(2) INFORMATION FOR SEQ ID NO: 4687:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 166 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:	
	TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA	60
	CTTAGTTGAA TTTGACGAAG AGTCTACAAA ANGTATTGTA ACTGGCGCAG TGAGCGATCA	120
40	TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA	166
	(2) INFORMATION FOR SEQ ID NO: 4688:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 189 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:	
	AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG	60
55		

	GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG	180
_	GTGACAAAC	189
5	(2) INFORMATION FOR SEQ ID NO: 4689:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 227 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:	
	TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG	60
	GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT	120
20	CTGGGCGTTA ACCCTAAGAN ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA	180
	CGAGGTCGTC GTCACTTAGA TTCTCATCTT GATACTGTGT GGTTGCG	227
25	(2) INFORMATION FOR SEQ ID NO: 4690:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 174 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:	
35	AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC	60
	GTCTTCAGTG TAAGCAACAG CATCTTCATT TNGCAGCCAA AATGCTTGGA TTATGTGCAA	120
	TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG	174
40	(2) INFORMATION FOR SEQ ID NO: 4691:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 363 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:	
	TTTTTTTTA AAAAAAGGGA AGGGAAAANA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT	60
	TTAAAGGGGG CCCAATTTTT CCCAAAAAAA AAACCCTTTG GGTTAAATTT TTTTTAAAAA	120
55		

	GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTT	240
5	TTAAGGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA	300
3	AAAATTAATT AAAnAACCCA TTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTTG	360
	GCC	363
10	(2) INFORMATION FOR SEQ ID NO: 4692:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 210 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:	
20	TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT	60
	ntttacttaa agtaaaatag aacacgattt tgatgtctgg gaatagtgga aatgataaaa	120
25	ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA	180
25	AAATAGGAAT ACATGAGTAA AACTCAnTGG	210
	(2) INFORMATION FOR SEQ ID NO: 4693:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 209 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:	
	ATAGTAGTAA AGTATTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT	60
40	CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT	120
	TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC	180
45	CCTCCACACA TAGCTACCCA GCTATCCGT	209
	(2) INFORMATION FOR SEQ ID NO: 4694:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 222 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	GCACATTAAC Chaagcacca GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG	60
	CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA	120
5	GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT	180
	ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG	222
10	(2) INFORMATION FOR SEQ ID NO: 4695:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 159 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:	
20	TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA	60
	TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT	120
	TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG	159
25	(2) INFORMATION FOR SEQ ID NO: 4696:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 161 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:	
	AATATGGTAG TTTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA	60
	ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT	120
40	TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A	161
	(2) INFORMATION FOR SEQ ID NO: 4697:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 170 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:	
	CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT	60
	CCRRICTOR INIGOTITY ITOOMS ORDERSHIP ASSIGNATIVE HILINIGHT	50

	ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA	170
	(2) INFORMATION FOR SEQ ID NO: 4698:	
5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 161 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:	
15	CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA	60
	TTGGGCGTAA ACGCGCGTAG GNGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA	120
	GGGTCATTGG AAACTGGAAA CTTGAGTCAG AAGAGGAAGT G	161
20	(2) INFORMATION FOR SEQ ID NO: 4699:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs  (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:	
	TAAATCTTCA TCAATATGAT CTAACCAATA TIGATAAAAC CTTGATGTGT TTCGTGTCAA	60
	TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT	120
35	GGGCAAGGTC ATCTTGCAAA ATGGATTCGA TTCAAGTGGG AGGGNCGATG ATGGACGTGC	180
	TGCATGCACT GATGACCCTT TTTGCCCATT CTGGCAAATC CCACCATGAA ATGACTGACG	240
	CGGACGCn	248
40	(2) INFORMATION FOR SEQ ID NO: 4700:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 175 base pairs	
45	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:	
	CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT	60
	GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT	120
<b>.</b>		

	(2) INFORMATION FOR SEQ ID NO: 4701:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 177 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:	
	TACAGGGTAG TGAGATTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT	60
15	AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT	120
	AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT	177
	(2) INFORMATION FOR SEQ ID NO: 4702:	
20 25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 156 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
23		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:	
30	CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA	60
	GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA	120
	GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG	156
35	(2) INFORMATION FOR SEQ ID NO: 4703:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 166 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:	
45	CTTGAAAAAG ATGGTTATTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT	60
	GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTNGTCAG CAAGACGCAC	120
50	AACGTCAAGC TGGTGTTGGT GCAGCAGTTG TAGCTGAATT AAGTGA	166
	(2) INFORMATION FOR SEQ ID NO: 4704:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs	

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	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:	
	GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG	60
10	ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT	120
	GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG	153
	(2) INFORMATION FOR SEQ ID NO: 4705:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 163 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:	
25	AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG	60
	AATGCCAATT AATTTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA	120
	nggaaacagc ccagaccacc agctaaggtc ccaaaatata tgt	163
30	(2) INFORMATION FOR SEQ ID NO: 4706:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 203 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:	
40	TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG	60
	CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGCA GTCGCGATGG	120
45	TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCn GTACCCGTCA GATATCCGCA	180
	GCAATGCAAT GTTGTGCAAG TTT	203
	(2) INFORMATION FOR SEQ ID NO: 4707:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 153 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:	
	CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTTCCAGA GGAGGCTCGT CCGCTCTGGG	60
5	TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG	120
	TACCACCTAT AATCGTTTTA ATCGATGGGG GGC	153
	(2) INFORMATION FOR SEQ ID NO: 4708:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 150 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:	
20	nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT	60
	AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG	120
	TATGTCTTTG GATAGAGTTA CAAACTTATT	150
25	(2) INFORMATION FOR SEQ ID NO: 4709:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 156 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:	
	AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA	60
	TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TNAGAGAATG TCATGATTAT	120
40	TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA	156
	(2) INFORMATION FOR SEQ ID NO: 4710:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 149 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:	
	GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC	60
		80

	TCGTTAAGGC TGAGCTGTGA TGGGGAGAA	149
	(2) INFORMATION FOR SEQ ID NO: 4711:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 160 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:	
15	TTGACTTCAA TACCATGGGC CAGGTACNCT TTAAATGTTG TTGTCTCAGT TAATATTAAT	60
	TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTCAG AATCTTTTTC	120
	AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG	160
20	(2) INFORMATION FOR SEQ ID NO: 4712:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 151 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:	
	ATAGTGAACC AGTACCGTGA GGACNAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA	60
	CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG	120
35	TAGAATGAAC CGGCGAGTTA CGATTTGATG C	151
	(2) INFORMATION FOR SEQ ID NO: 4713:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 145 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:	
	ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC	
	CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGNGGGTA GCGGAGAAAT TCCAATCGAA	60
50	CCTGGGAGAT AGCTGGTTCT CTCCG	120
	(2) INFORMATION FOR SEQ ID NO: 4714:	145
	(2) INTOGENITOR FOR BEG ID NO: 4/14:	

5	<ul><li>(A) LENGTH: 151 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:	
10	TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA	60
	TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA	120
	AAACCGACAG GCCTTAACGG GCCGCGGGG T	151
15	(2) INFORMATION FOR SEQ ID NO: 4715:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 151 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:	
	TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	60
	GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA	120
30	CTTTAAAAAA ATAAGACACT TTGCCAACTT G	151
	(2) INFORMATION FOR SEQ ID NO: 4716:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 152 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:	
	GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT	60
45	TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA	120
	TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC	152
	(2) INFORMATION FOR SEQ ID NO: 4717:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 144 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:	
	GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA	60
5	ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA	120
	CGAACTTGTC CAAGGATTAC GAAA	144
10	(2) INFORMATION FOR SEQ ID NO: 4718:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 145 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:	
20	ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC	60
	AACTTAGAGT GCCCAACTNA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA	120
	CTTAACCCAA CATCTCACGA CACGA	145
25	(2) INFORMATION FOR SEQ ID NO: 4719:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 156 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:	
	AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT	60
	CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACTGTA ATGGTGTCGT	120
40	ACAChATGCC ATTTAAAAAT AGCATACCGG CAAAGC	156
	(2) INFORMATION FOR SEQ ID NO: 4720:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 152 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:	
	TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC	60

	TAACTCGGAT CAAATTCGTC TCGATGACCT GG	152
	(2) INFORMATION FOR SEQ ID NO: 4721:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 146 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:	
15	CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT	60
	TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG	120
	TTACAGCTAT CTTAGCTAGT TTAGCC	146
20	(2) INFORMATION FOR SEQ ID NO: 4722:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 156 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:	
	CCACACCAAT ATTTTGCGCT AAGTANATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC	60
	CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC	120
35	TAACATTACC CAGCCATACA GCCATACCAG GGCCAC	156
	(2) INFORMATION FOR SEQ ID NO: 4723:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 161 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:	
	ACGGTCTTGC TGTCACTTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn	60
50	GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG	120
	AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A	161
	(2) INFORMATION FOR SEQ ID NO: 4724:	

5	<ul><li>(A) LENGTH: 165 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:	
10	CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA	60
	TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA	120
	ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA	165
15	(2) INFORMATION FOR SEQ ID NO: 4725:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 149 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:	
	GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA	60
	CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT	120
30	GACATGTGGA GCTGGACGAA TACTAATCG	149
	(2) INFORMATION FOR SEQ ID NO: 4726:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 275 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:	
	TTGAATTTTT GAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA	60
45	ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT	120
, 0	GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT	180
	CAGCATGCCG GTGTTCCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA	240
50	GAnCGGTAAA GTAGACANCG GTAGTATACT GAAAT	275
	(2) INFORMATION FOR SEQ ID NO: 4727:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:	
	ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT	60
10	AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA	120
	TGCATTCTAT GATGCTTCTA ACTGAATnA	149
	(2) INFORMATION FOR SEQ ID NO: 4728:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 158 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:	
25	GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA	60
23	TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT	120
	GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG	158
30	(2) INFORMATION FOR SEQ ID NO: 4729:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 138 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:	
	TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCG ATCTGGACCA TATTTTTTTA	60
	TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT	120
45	GCCCTCCCAT ACCTCGGG	138
	(2) INFORMATION FOR SEQ ID NO: 4730:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 187 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCGG ATTTGTCTGA ATTCGTAACC	60
5	GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT	120
J	AAAGTATTTC GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA	180
	GTTCATC	187
10	(2) INFORMATION FOR SEQ ID NO: 4731:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 137 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:	
20	CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA	60
	AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCCTAT CCGTCGTGGG CGTAGGAAAT	120
25	TTnAGAGGAG CTGTCCT	137
25	(2) INFORMATION FOR SEQ ID NO: 4732:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 137 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:	
	TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA	60
	TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATTTTT	120
40	TCTTCAACTA AGTCACG	137
	(2) INFORMATION FOR SEQ ID NO: 4733:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 137 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:	
	TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA	60
55		

	TCTTCAACTA AGTCACG	137
	(2) INFORMATION FOR SEQ ID NO: 4734:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 153 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:	
15	AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA	60
	ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG	120
	ACAAAATTTA TTTCGTCGTC CCACCCCAAC TTG	153
20	(2) INFORMATION FOR SEQ ID NO: 4735:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 142 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:	
	TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATNATTGC	60
	AAGCTGACTT TTCGTCACTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG	120
35	TACTTTGATT GATGTCCAAG TT	142
	(2) INFORMATION FOR SEQ ID NO: 4736:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 137 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:	
	ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT	60
50	TTTTGTAACT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC	120
	ATCAATCCAA GCTTTTG	137
	(2) INFORMATION FOR SEQ ID NO: 4737:	

5	<ul><li>(A) LENGTH: 144 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:	
10	GGTCGTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA	60
	AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAnT GAGCGGATGA	120
	ACTGAGGGTA GCGGAGAAAT TCCA	144
15	(2) INFORMATION FOR SEQ ID NO: 4738:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 157 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:	
	GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA	60
	TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG	120
30	GAACATGGTG ACATGTMATC TGCTTTTCTA ATCATAC	157
	(2) INFORMATION FOR SEQ ID NO: 4739:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 145 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:	
	GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT	60
45	GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAMATG	120
	AGTAAGTGAG AGCCGAAGAG AGGGA	145
	(2) INFORMATION FOR SEQ ID NO: 4740:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 234 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:	
	TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT	60
5	CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG	120
	TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT	180
	GAGACCCACG TTCAACTTGC CNGCACGTTC TACTCTGCGG ANTAGTGGCT ACCA	234
10	(2) INFORMATION FOR SEQ ID NO: 4741:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 135 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:	
	GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA	60
	TGGTCAAAAT ATATTGTTGT CATTTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA	120
25	TCATGATACT GTCAn	135
	(2) INFORMATION FOR SEQ ID NO: 4742:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 145 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:	
	ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	60
40	AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GANAGCTGGT	120
	TCTCTCCGAA ATAGCTTTAG GGCTA	145
1 <i>E</i>	(2) INFORMATION FOR SEQ ID NO: 4743:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 151 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:	

	TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA	120
	TCTTAAACTT AGTTATGGTA TGTGGCGTCA A	151
5	(2) INFORMATION FOR SEQ ID NO: 4744:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 132 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:	
	TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC	60
	AGGCGATAAA ATCANAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA	120
20	TTATGTACAA CA	132
	(2) INFORMATION FOR SEQ ID NO: 4745:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 132 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:	
	CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC	60
35	TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT	120
	AGAAAGGAGG TG	132
	(2) INFORMATION FOR SEQ ID NO: 4746:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 138 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:	
_	GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA	60
50	GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC	120
	GACAnTGACT CGGATTCA	138

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 185 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:	
10	CATTATTGTA AACTGAACTT TTCGTCACTT GCTGGTGnTT GGGGACCCCA CCAACTTGGC	60
	ACATTATTGG TAAGCTGACT TTTCGTCACT TACTGTGTTG GGGCCCCGCC AACTTGCATT	120
15	GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT	180
	GCCTG	185
	(2) INFORMATION FOR SEQ ID NO: 4748:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 173 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:	
	ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT	60
30	ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA	120
	AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG	173
	(2) INFORMATION FOR SEQ ID NO: 4749:	
35	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 212 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
40	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:	
45	ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC	60
	CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT	120
	AATTAAAGGG CATGCAACCA AGTANCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT	180
50	TGNTAAATAC GGTGTTTGAC AATTGCGCAC CT	212
	(2) INFORMATION FOR SEQ ID NO: 4750:	

5	<ul><li>(A) LENGTH: 140 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:	
10	AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAAG CTTGAATTCA	60
	TAAGAAATAA TCGCTAGTGT TCGAAAGACN GCAGCAAGAT TAATAACGCG TTTAAATCTT	120
	TTTATAAAAG AAAACGTTTA	140
15	(2) INFORMATION FOR SEQ ID NO: 4751:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 184 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:	
	ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT	60
	GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT	120
30	TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA	180
	TCCG	184
35	(2) INFORMATION FOR SEQ ID NO: 4752:	
33	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 133 base pairs  (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:	
45	GGGATCTTCC GCAATGGGCG AAACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT	60
	CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTNA	120
	CGGTACCTAA TCA	133
50	(2) INFORMATION FOR SEQ ID NO: 4753:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 162 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:	
	GTATGCTGTG TGGCTTGTCA TGTTCGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT	60
5	ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT	120
	TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG	162
10	(2) INFORMATION FOR SEQ ID NO: 4754:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 134 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:	
20	AATTCGATTC CCTTAGTAGC GGCGACGAAA ACGGGAANGA GCCCAAACCA ACAAGCTTGC	60
	TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT	120
25	CTTGGGAAAG ATGA	134
	(2) INFORMATION FOR SEQ ID NO: 4755:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 139 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:	
	AGAGTGCGTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC	60
	ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT	120
40	TGAAGCATGn ATCGTAAGG	139
	(2) INFORMATION FOR SEQ ID NO: 4756:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 163 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:	

	CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA	120
5	ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA	163
5	(2) INFORMATION FOR SEQ ID NO: 4757:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 160 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:	
	CATGAAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG	60
	TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACANGAT	120
20	TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA	160
	(2) INFORMATION FOR SEQ ID NO: 4758:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 177 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:	
	TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG	60
35	GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT	120
	ACTGCTGTTC TCTATTTATA CCANATTACT TTCGTAATTG TTAAAATTTT AAAAGGA	177
40	(2) INFORMATION FOR SEQ ID NO: 4759:  (i) SEQUENCE CHARACTERISTICS:	
	<ul><li>(A) LENGTH: 127 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
45	(a)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:	
50	CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG	60
	ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACTTATGGG	120
	ATTTGCT	127
55		

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 145 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:	
	GGGCCCCTCG TCGGGTTACC GAATTCAGAC AAACTCCGnA ATGCCAATTA ATTTAACTTG	60
	GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA	120
15	AGTCCCAAAT ATATGTTAAT GAAAG	145
	(2) INFORMATION FOR SEQ ID NO: 4761:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 228 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:	
	TAAACAAGGC GCGTTGGGCC TATTCACTGC GGCTCTTCTG GGCGTTAACC CTAAAGAGCA	60
30	CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA	120
	CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA	180
	TTAACACACC AAAACAGCTC CCACCACCAC TANATCGANC AACACTAG	228
35	(2) INFORMATION FOR SEQ ID NO: 4762:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 130 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:	
	TNGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT	60
	ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC	120
50	AGCAGGGTTG	130
	(2) INFORMATION FOR SEQ ID NO: 4763:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 151 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:	
	CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG	60
10	GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA	120
	GTTCACATCG ACGGGGAGGT TTGGCACCTC G	151
	(2) INFORMATION FOR SEQ ID NO: 4764:	
15 20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 128 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:	
25	ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC	60
	CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC	120
	TACTGCCA	128
30	(2) INFORMATION FOR SEQ ID NO: 4765:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 135 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:	
	AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC	60
	TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC	120
45	TTTCCATGTG GnAAC	135
	(2) INFORMATION FOR SEQ ID NO: 4766:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 126 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT	60
	CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC	120
5	CACAGC	126
	(2) INFORMATION FOR SEQ ID NO: 4767:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 13C base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: Couble  (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:	
	TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACNTCATTC GAGTACTGTC	60
20	ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT	120
	GATTTTAAC	130
	(2) INFORMATION FOR SEQ ID NO: 4768:	
25 30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 142 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:	
35	GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA	60
	ANGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG	120
	TAGGGCACCT ATTTTCCTAT CT	142
40	(2) INFORMATION FOR SEQ ID NO: 4769:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 136 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:	
50	CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC	60
	CGTCGATGTG AACTCTTGNG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC	120

	(2) INFORMATION FOR SEQ ID NO: 4770:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 145 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:	
	CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA	60
15	ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA	120
	TAGAGCTATT AAGCGTnGCC ATGAG	145
	(2) INFORMATION FOR SEQ ID NO: 4771:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 128 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:	
30	TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT	60
	GTGCCTTTGG AAATGGTGAG GNGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC	120
	ATGTGGGA	128
35	(2) INFORMATION FOR SEQ ID NO: 4772:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 126 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:	
	GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA	60
	ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT	120
50	GTACTT	126
	(2) INFORMATION FOR SEQ ID NO: 4773:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs	

(b) TOPOLOGI: Tilleat	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:	
GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT	60
GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAN ACCTTGCGGT CTCAATGCGG	120
CTCATC	126
(2) INFORMATION FOR SEQ ID NO: 4774:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 124 base pairs  (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:	
ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC	60
TGCATCTTNA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT	120
TACG	124
(2) INFORMATION FOR SEQ ID NO: 4775:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 124 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:	
ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC	60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGANCCAGAA ACTCCAACAC CGCCAACACC	120
AGAG	124
(2) INFORMATION FOR SEQ ID NO: 4776:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 135 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	GTCTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAN ACCTTGCGGT CTCAATGCGG CTCATC  (2) INFORMATION FOR SEQ ID NO: 4774:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:  ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC TGCATCTTNA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT TACG  (2) INFORMATION FOR SEQ ID NO: 4775:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:  ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAACGT AGCCGGAAAC ACCAACACCA CCGACACCAG AAGTGCCGAG TGANCCAGAA ACTCCAACAC CGCCAACACC AGAG  (2) INFORMATION FOR SEQ ID NO: 4776:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

	CCCGCTAGTC TCCACCATTT ATTTTTACA CGATGAACAT TGAAAACTNA ATACAATATG	60
	CAACGTTAAT TCCAAAAAAC GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT	120
5	AATCAAACAT CATAA	135
	(2) INFORMATION FOR SEQ ID NO: 4777:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 144 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:	
	AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA	60
20	GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG	120
	TTGGGGGTTC AAACAGGATT TAGA	144
25	(2) INFORMATION FOR SEQ ID NO: 4778:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 123 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:	
35	AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG	60
	TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC	120
	ССТ	123
40	(2) INFORMATION FOR SEQ ID NO: 4779:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 127 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:	
	GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG	60
	AACAATATAG CTCAGGTATT ACGTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC	120
55		

	(2) INFORMATION FOR SEQ ID NO: 4780:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 127 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:	
	GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCANTGTC CTCGACTAGT GAGCTATTAC	60
15	GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA	120
	TCCTTTT	127
	(2) INFORMATION FOR SEQ ID NO: 4781:	
20 25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 129 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:	
30	ACACNGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT	60
	GTCTTATTTT TTTAAAGTAT TTAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG	120
	CGAGACTCC	129
35	(2) INFORMATION FOR SEQ ID NO: 4782:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 136 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:	
	CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT	60
	AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTCAT GTTTGnTTTG	120
50	GTCAGATTTA GGACCA	136
	(2) INFORMATION FOR SEQ ID NO: 4783:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:	
	CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC	60
10	AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG	119
	(2) INFORMATION FOR SEQ ID NO: 4784:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 127 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:	
	ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT	60
25	nATCCCATTG CATCCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG	120
	CGCACGG	127
	(2) INFORMATION FOR SEQ ID NO: 4785:	
<i>30</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 119 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:	
40	ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG	60
	ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT	119
	(2) INFORMATION FOR SEQ ID NO: 4786:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 137 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:	
55	CTTTCTAAAC CCGnCACCAC TTTATCGTGG TGGGGAGACA GTGTTCAGGC GGGCCAGTTT	60

	AATCATTCAT AGAGTGT	137
_	(2) INFORMATION FOR SEQ ID NO: 4787:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 119 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:	
15	GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT	60
	TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT	119
	(2) INFORMATION FOR SEQ ID NO: 4788:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 141 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:	
	CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT	60
30	TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCG	
		120
	GCCACATA GCTACCCAGC T	141
35	(2) INFORMATION FOR SEQ ID NO: 4789:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 139 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:	
	CTGGGTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG	60
	AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT	120
50	GCCAACGCAT AGCTGGGTA	139
	(2) INFORMATION FOR SEQ ID NO: 4790:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs	

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:	
	·	
	CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG	60
10	GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG	120
	CTTGCTTCG	129
	(2) INFORMATION FOR SEQ ID NO: 4791:	
15 20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 120 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:	
25	GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT	60
	TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC	120
	(2) INFORMATION FOR SEQ ID NO: 4792:	
<i>30 35</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 123 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:	
40	CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC	60
	AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC	120
	CGn	123
45	(2) INFORMATION FOR SEQ ID NO: 4793:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 130 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:	

	AGTTTTGAAT GTTTGTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC	120
	nCCTGATAAC	130
5	(2) INFORMATION FOR SEQ ID NO: 4794:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 115 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:	
	CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT	60
	TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT	115
20	(2) INFORMATION FOR SEQ ID NO: 4795:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 224 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:	
	nttaaaaaaa attcccaatt ttttttgggg ggttgggaat ttaaaaattt ggttttaac	60
	CCAAAGGCCC TTTTCCCAAA AATTTAAATT CCCTTAAAAA TTTAAAATTT GGGAATTTTT	120
35	TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTAATT TAACCCTTAA	180
	AACCCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA	224
	(2) INFORMATION FOR SEQ ID NO: 4796:	
40	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 120 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:	
50	TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCANGAT	60
	GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGCAGAT	120
55	(2) INFORMATION FOR SEQ ID NO: 4797:	

5	<ul><li>(A) LENGTH: 125 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:	
10	AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG	60
	CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC	120
	ATCTG	125
15	(2) INFORMATION FOR SEQ ID NO: 4798:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 113 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:	
	CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT	60
	AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC	113
30	(2) INFORMATION FOR SEQ ID NO: 4799:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 116 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:	
	CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA	60
	AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG	116
45	(2) INFORMATION FOR SEQ ID NO: 4800:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 112 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:	

	TCAGTGCGAT GATTCGTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT	112
	(2) INFORMATION FOR SEQ ID NO: 4801:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 110 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:	
15	ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA	60
	ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC	110
	(2) INFORMATION FOR SEQ ID NO: 4802:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 237 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:	
	GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT	60
30	TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC	120
	CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATNCTTA	180
35	CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA	237
	(2) INFORMATION FOR SEQ ID NO: 4803:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 114 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:	
	CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC	60
50	AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG	114
	(2) INFORMATION FOR SEQ ID NO: 4804:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:	
	GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT	60
10	GTTAGGGGTT TCCGCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT	113
	(2) INFORMATION FOR SEQ ID NO: 4805:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:	
	TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA	60
25	CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT	108
	(2) INFORMATION FOR SEQ ID NO: 4806:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 115 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:	
	TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT	60
40	GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGANAGCTC CTCTC	115
	(2) INFORMATION FOR SEQ ID NO: 4807:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 167 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:	
	CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA	60
55	TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT	120

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808: TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC ATCATTGCTA GCTTTTCTTG TATTAACTGA TANTTCTAA TTGGTTTGCC GAATTGCT (2) INFORMATION FOR SEQ ID NO: 4809: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809: TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC TCCTATACCT CAGTTCATCC GCTCACTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG TACCTGACTT CAACTGACCA GGGTAGACAC (2) INFORMATION FOR SEQ ID NO: 4810: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810: AAGAAGGCGA CGATACATTA TCACCTGGT TAACAATTAG TACGTGTATA TATCGTTCAN AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA (2) INFORMATION FOR SEQ ID NO: 4811: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (XI) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		(2) INFORMATION FOR SEQ ID NO: 4808:	
TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCATTGC TTGCAGCTAA ATTACCTTGC  ATCATTGCTA GCTTTTCTTG TATTAACTGA TANTACTAA TTGGTTTGCC GAATTGCT  (2) INFORMATION FOR SEQ ID NO: 4809:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDENDESS: double (D) TOPOLOGY: linear  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:  TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC  TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAGGGGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double	5	<ul><li>(A) LENGTH: 118 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
ATCATTGCTA GCTTTTCTTG TATTAACTGA TANTTACTAA TTGGTTTGCC GAATTGCT  (2) INFORMATION FOR SEQ ID NO: 4809:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:  TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC  TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  40  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGGAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:	
(2) INFORMATION FOR SEQ ID NO: 4809:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:  TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTCGAATTTC  TCCNATACCT CAGTTCATCC GCTCACTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  40  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC	60
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809: TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC (2) INFORMATION FOR SEQ ID NO: 4810: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810: AAGCGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA (2) INFORMATION FOR SEQ ID NO: 4811: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	15	ATCATTGCTA GCTTTTCTTG TATTAACTGA TANTTACTAA TTGGTTTGCC GAATTGCT	118
(A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:  TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  40  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGGAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACCTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(2) INFORMATION FOR SEQ ID NO: 4809:	
TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC  TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	20	<ul><li>(A) LENGTH: 150 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG  TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS:	25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:	
TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC	60
TACCTGACTT CAACTGACCA GGGTAGACAC  (2) INFORMATION FOR SEQ ID NO: 4810:  (i) SEQUENCE CHARACTERISTICS:	20	TCCNATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG	120
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAn  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	30	TACCTGACTT CAACTGACCA GGGTAGACAC	150
(A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(2) INFORMATION FOR SEQ ID NO: 4810:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:  AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	35	<ul><li>(A) LENGTH: 107 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAN  AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	40		
AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:	
AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA  (2) INFORMATION FOR SEQ ID NO: 4811:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double		AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAn	60
(i) SEQUENCE CHARACTERISTICS:  50 (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	45	AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA	107
(A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(2) INFORMATION FOR SEQ ID NO: 4811:	
	50	<ul><li>(A) LENGTH: 117 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:	
	AGAGTGNATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCG AGGAAGACAC	60
5	AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA	117
	(2) INFORMATION FOR SEQ ID NO: 4812:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 123 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:	
	CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATNACTA AATCCGTCTT	60
20	TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA	120
	ATG	123
	(2) INFORMATION FOR SEQ ID NO: 4813:	
25 30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 106 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:	
35	TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC	60
	TAGCCCTAAA GCTATTTCGG AGAGAACCAG CTATCTCCAG GTTCGA	106
	(2) INFORMATION FOR SEQ ID NO: 4814:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 112 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:	
	CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG	60
50	GAATCGCGAA CGTTGGCCAACGA TTGGCGTGGG AATCATCCAG TG	112
	(2) INFORMATION FOR SEQ ID NO: 4815:	

5	<ul><li>(A) LENGTH: 125 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:	
10	ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGCACCA	60
	TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT	120
	AGGTT	125
15	(2) INFORMATION FOR SEQ ID NO: 4816:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 104 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:	
	GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATTA AATGAAGATG	60
	CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT	104
30	(2) INFORMATION FOR SEQ ID NO: 4817:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:	
40	GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG	60
	ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG	117
45	(2) INFORMATION FOR SEQ ID NO: 4818:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 121 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:	

	TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC	120
	A	121
5	(2) INFORMATION FOR SEQ ID NO: 4819:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 118 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:	
	TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG	60
	TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTNAAGA	118
20	(2) INFORMATION FOR SEQ ID NO: 4820:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 104 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:	
30	CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCGGAG	60
	AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC	104
35	(2) INFORMATION FOR SEQ ID NO: 4821:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 165 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(D) TOPOLOGI: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:	
45	TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA	60
	TTATTTTAAA TGCTCATTTA CATAGTNAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT	120
	AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT	165
50	(2) INFORMATION FOR SEQ ID NO: 4822:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs	
55		

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:	
	GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG	60
10	AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG	113
	(2) INFORMATION FOR SEQ ID NO: 4823:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 106 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:	
	CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC	60
25	TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC	106
25	(2) INFORMATION FOR SEQ ID NO: 4824:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 108 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:	
	TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC	60
	CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACTAGAGn	108
40	(2) INFORMATION FOR SEQ ID NO: 4825:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 116 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:	
	TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG	60
	nTGTAAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT	116
55		

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 160 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:	
	ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA	60
	ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA	120
15	ATCCTTGTAT TGCGTGTCAT ANAGTCTTTG CTCCTTGCAC	160
	(2) INFORMATION FOR SEQ ID NO: 4827:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 115 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:	
	CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC	60
30	AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC	115
	(2) INFORMATION FOR SEQ ID NO: 4828:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 103 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:	
	CCAAAATAGC CTTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT	60
45	TCAGAAAGCT TTTGATTAAC TTTAAAGTAT nCCCAATTAT AAT	103
	(2) INFORMATION FOR SEQ ID NO: 4829:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 111 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	GGACCGAACT GTCTCACGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA	60
	GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A	111
5	(2) INFORMATION FOR SEQ ID NO: 4830:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 105 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:	
	GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT	60
	TTTCGTTCAG TCAACNACTG CCAATATAAC TTTGTAGAGC ATTGA	105
20	(2) INFORMATION FOR SEQ ID NO: 4831:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 102 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:	
30	ACATTGAGTC TTCGAGTCGT TGCATTTCAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT	60
	AGGTGCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA	102
35	(2) INFORMATION FOR SEQ ID NO: 4832:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 107 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:	
45	TTnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG	60
	TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC	107
50	(2) INFORMATION FOR SEQ ID NO: 4833:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 144 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:	
5	TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT	60
5	CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA	120
	TTTTCAGCAT CAATTTGATC AATC	144
10	(2) INFORMATION FOR SEQ ID NO: 4834:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 108 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:	
20	GGCTCAGATG NACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA	60
	GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG	108
25	(2) INFORMATION FOR SEQ ID NO: 4835:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 102 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:	
35	GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG	60
	CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT	102
	(2) INFORMATION FOR SEQ ID NO: 4836:	
40 45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 109 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:	
50	TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG	60
	TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAAA	109

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 103 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:	
	CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC	60
	CGGAATTTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC	103
15	(2) INFORMATION FOR SEQ ID NO: 4838:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 121 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:	
	TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT	60
	GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG	120
30	A	121
	(2) INFORMATION FOR SEQ ID NO: 4839:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 104 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:	
	AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT	60
45	ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG	104
	(2) INFORMATION FOR SEQ ID NO: 4840:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 127 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC	60
5	TTGAAACGTG AGCGCTATTA GTGNAGGCGT GGTGGGTACT ACCCTAGCTG TGTTGGCTTT	120
	CTAACCC	127
	(2) INFORMATION FOR SEQ ID NO: 4841:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 125 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:	
00	CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT	60
20	CATTCAGTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTTAT TAGTGTTTCA	120
	GTTCT	125
25	(2) INFORMATION FOR SEQ ID NO: 4842:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 108 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:	
35	TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTANGCGCTC	60
	CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC	108
40	(2) INFORMATION FOR SEQ ID NO: 4843:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:	
50	TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGAA GGAACATGTG TGTAAGTAGC	60
	TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT	108
	(2) INFORMATION FOR SEQ ID NO: 4844:	
55		

5	<ul><li>(A) LENGTH: 117 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:	
10	CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG	60
	AACCTAAGTT GGGCTACCAT CGACGNCTAA GAACCTTTCT TGACTTGTGT ACAATCG	117
	(2) INFORMATION FOR SEQ ID NO: 4845:	
15 20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:	
25	GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG	60
	CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA	108
	(2) INFORMATION FOR SEQ ID NO: 4846:	
30 35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 118 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:	
40	CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC	60
40	AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT	118
	(2) INFORMATION FOR SEQ ID NO: 4847:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 104 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:	
	GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA	60
55		

	(2) INFORMATION FOR SEQ ID NO: 4848:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 137 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:	
	CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC	60
15	CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG	120
	CCAGCAACGC GATTACC	137
	(2) INFORMATION FOR SEQ ID NO: 4849:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 116 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:	
	GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG	60
30	TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACANGGGGGG GGGGGG	116
	(2) INFORMATION FOR SEQ ID NO: 4850:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 125 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:	
	TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG	60
45	TTATAGTTAC GGTCCGCCGT TTACTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA	120
	СТССТ	125
	(2) INFORMATION FOR SEQ ID NO: 4851:	
50	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 96 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:	
5	AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC	60
	TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC	96
	(2) INFORMATION FOR SEQ ID NO: 4852:	
10 15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 100 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:	
	ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGNAT	60
20	GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG	100
	(2) INFORMATION FOR SEQ ID NO: 4853:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 101 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:	
	CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTA	60
35	ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T	101
	(2) INFORMATION FOR SEQ ID NO: 4854:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 102 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:	
	GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG	60
50	GTGAAANACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT	102
	(2) INFORMATION FOR SEQ ID NO: 4855:	

5	<ul><li>(A) LENGTH: 104 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:	
10	ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA	60
	CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG	104
	(2) INFORMATION FOR SEQ ID NO: 4856:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 138 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:	
	CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT	60
25	TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC	120
	CATCTCCTTA ACCCGGTA	138
30	(2) INFORMATION FOR SEQ ID NO: 4857:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 100 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:	
40	TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA	60
	TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC	100
	(2) INFORMATION FOR SEQ ID NO: 4858:	200
45	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:	
	And onformer processions ond in MA: 4030:	

	CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCACTG CGGCTT	106
	(2) INFORMATION FOR SEQ ID NO: 4859:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 152 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:	
15	GTAACTCGCC GGTTCATTCT ACAAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA	60
7.5	CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCCTTT CCGGGGTnGC	120
	TTTTTCAACC TTTTTCCCCC TCCACGGTTA CT	152
20	(2) INFORMATION FOR SEQ ID NO: 4860:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 100 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:  GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGANGAA TTCTAAGGTG AGCGAGCGAA	60
	CTCTCGTTAA GGAACTCGGC AAACTGACCC CGTCACTTCG	100
	(2) INFORMATION FOR SEQ ID NO: 4861:	
<i>35 40</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 104 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:	
45	CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA	60
	AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT	104
	(2) INFORMATION FOR SEQ ID NO: 4862:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 87 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:	
-	TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA	60
5	CCTCCTGCGT GCAAAGCAGG CGCTCTG	87
	(2) INFORMATION FOR SEQ ID NO: 4863:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 105 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:	
	ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGG	60
20	CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAMTTTTCA ATGTA	105
	(2) INFORMATION FOR SEQ ID NO: 4864:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 129 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:	
	AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG	60
35	TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT	120
	GCAntggct	129
40	(2) INFORMATION FOR SEQ ID NO: 4865:	
70	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 100 base pairs  (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:	
50	AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC	60
	TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC	100

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 115 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:	
	GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT	60
	TATTTTAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT	119
15	(2) INFORMATION FOR SEQ ID NO: 4867:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 90 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
20	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:	
	ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA	60
	CGGTTTAGCA GAGACCTGTG TTTTTGATAA	90
30	(2) INFORMATION FOR SEQ ID NO: 4868:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 87 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:	
40	CACGAACGAT TGTCTTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC	60
	GCTACTGCTC ATCAGGGATT ACAAACC	87
45	(2) INFORMATION FOR SEQ ID NO: 4869:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 165 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
50	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 4869:	

	CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT	120
	AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA	165
5	(2) INFORMATION FOR SEQ ID NO: 4870:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 111 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:	
	AATATCATTT ATAACATTAA GTAATAACTT TTTTTATCTT GTCCATTTTA TTTTTNAACC	60
	AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G	111
20	(2) INFORMATION FOR SEQ ID NO: 4871:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 84 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:	<b>60</b>
	TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCACTG CGGCTCTTCT	60
	GGGCGTTAAC CCTAAAGAGC ACCC	84
35	(2) INFORMATION FOR SEQ ID NO: 4872:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 101 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:	
45	ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT	60
	ATGATTTCAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C	101
50	(2) INFORMATION FOR SEQ ID NO: 4873:	
55	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 87 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:	
5	GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC	60
J	GATGGGGGGA AGCATAGGAT AGGCGAA	87
	(2) INFORMATION FOR SEQ ID NO: 4874:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 81 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:	
	GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTCG ATCCCGCTAG TCTCCACCAT	60
20	TATTTGTACA TTGAAAACTA G	81
	(2) INFORMATION FOR SEQ ID NO: 4875:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 81 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:	
	TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG	60
35	CGAACTGAAT AAATAAAGAT T	83
	(2) INFORMATION FOR SEQ ID NO: 4876:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 87 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:	
	AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG	60
50	TGGAACATAG ATTAAGTTAT TAAGGGC	87
	(2) INFORMATION FOR SEQ ID NO: 4877:	

5	<ul><li>(A) LENGTH: 101 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:	
10	ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA	60
	CGGGGAGGTT TGnCCTCAAT GTGGCTCATC GGATCTTGGG G	101
	(2) INFORMATION FOR SEQ ID NO: 4878:	
15	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 79 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:	
25	ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT	60
	CAACTGCATG AGGTATATT	79
	(2) INFORMATION FOR SEQ ID NO: 4879:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 83 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:	
40	ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA	60
	AAATTGGTAT GGTAATTGTG GCA	83
	(2) INFORMATION FOR SEQ ID NO: 4880:	
<i>45 50</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 84 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:	
	CTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA	
55	CITCHICCIG RICCHGAICA AMCICICCAI AMAMAITAIG AIGITIGATI AGCTCATAGA	60

	(2) INFORMATION FOR SEQ ID NO: 4881:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 80 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:	
	TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG	60
	CTTCACGCTT CTTCGCATTA	80
15	(2) INFORMATION FOR SEQ ID NO: 4882:	00
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 86 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:	
	TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAACTTGAGT	60
30	GCAGAAGAGG AAAGTGGGTT CCATGT	86
	(2) INFORMATION FOR SEQ ID NO: 4883:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 127 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:	
	TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA	60
	AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT	120
45	CGGTTAA	127
	(2) INFORMATION FOR SEQ ID NO: 4884:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:	
	AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC	60
5	CTATTAAAAA TAATAAAT	78
	(2) INFORMATION FOR SEQ ID NO: 4885:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 84 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:	
	CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT	60
20	GTGGATTGTC CTTTGGAAAT GGGT	84
	(2) INFORMATION FOR SEQ ID NO: 4886:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 117 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:	
	GGTATCTGTT CACTCTTCCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT	60
35	TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAAnTGG TACCCCATCC AAAAGGG	117
	(2) INFORMATION FOR SEQ ID NO: 4887:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 80 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:	
	CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT	60
50	ACCGTGAGGA AAGGTGAAAA	80
	(2) INFORMATION FOR SEQ ID NO: 4888:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs	
7.7		

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:	
	AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA	60
10	GGCCTTACGT TTGCGTG	77
	(2) INFORMATION FOR SEQ ID NO: 4889:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 76 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:	
	TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTTGCCGA	60
	GTTCCTTAAC GAGAGT	76
25	(2) INFORMATION FOR SEQ ID NO: 4890:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:	
	GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATNATGTG GCAAGTTGGC	60
	GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT	117
40	(2) INFORMATION FOR SEQ ID NO: 4891:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 109 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891: TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA	60
	CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA	109
55		

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 88 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:	
	CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG	60
	AGACCGTGTG TTTTTGAGAA ACAGGTGC	88
15	(2) INFORMATION FOR SEQ ID NO: 4893:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 102 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893: TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCG GCAGTTCGAA	
		60
	TCTGCCCCCC TCCATTTATT ATTTTNAAAA AAAGCATAGT TC	102
30	(2) INFORMATION FOR SEQ ID NO: 4894:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:	
40	CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT	60
	GACTCAGATT CCGACAGT	78
	(2) INFORMATION FOR SEQ ID NO: 4895:	
<i>45 50</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 141 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:	

	TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC	120
	TTATACCGAG TnGGAATCTC A	141
5	(2) INFORMATION FOR SEQ ID NO: 4896:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 80 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:	
	GTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTCAGA AGCCATTTTA TGAAAAGAGT	60
	GATTTAATTC ATAAATTTCT	80
20	(2) INFORMATION FOR SEQ ID NO: 4897:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 73 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897: GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC	60
	AAACCAATTA GTA	73
35	(2) INFORMATION FOR SEQ ID NO: 4898:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 71 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:	
45	GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG	60
40		71
	TGCGTCTGCC A  (2) INFORMATION FOR SEQ ID NO: 4899:	
50		
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 116 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:	
5	AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT	60
3	TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT	116
	(2) INFORMATION FOR SEQ ID NO: 4900:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 113 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:	
	TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC	60
20	CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC	113
	(2) INFORMATION FOR SEQ ID NO: 4901:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:	
	ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT	60
35	AAAAATAGGG AATACATG	78
	(2) INFORMATION FOR SEQ ID NO: 4902:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 84 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:	
	ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT	60
	CAAAACTAGA TAGTAAGTAA AAGT	84
50	(2) INFORMATION FOR SEQ ID NO: 4903:	

	<ul><li>(A) LENGTH: 70 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
5	12, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:	
10	TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG	60
10	AGACTCGGTG	70
	(2) INFORMATION FOR SEQ ID NO: 4904:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 151 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:	
25	TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT	60
	TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTTGTTGT AATAAGTTAT	120
	GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A	151
30	(2) INFORMATION FOR SEQ ID NO: 4905:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 75 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:	
40	TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC	60
	TTATCGTGGT GGGGA	75
45	(2) INFORMATION FOR SEQ ID NO: 4906:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 112 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:	

	ACTCAGACAG TGACTCAGAT CAGATAGTGN CTCGGATTCA GCGATTATTC AG	112
	(2) INFORMATION FOR SEQ ID NO: 4907:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 70 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:	
15	GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA	60
	AGGTTTACCA	70
	(2) INFORMATION FOR SEQ ID NO: 4908:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 121 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:	
30	AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTC GGTGGGACAC AATAGTGTTG	60
	ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC	120
	c	121
35	(2) INFORMATION FOR SEQ ID NO: 4909:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 70 base pairs  (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:	
40	GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG	60
	TTAAGTCCCG	70
50	(2) INFORMATION FOR SEQ ID NO: 4910:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 100 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
55	(0)	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:	
	GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG	60
5	TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG	100
	(2) INFORMATION FOR SEQ ID NO: 4911:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 155 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:	
	nTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAAATAAC	60
20	TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACTTTGAT	120
	GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTCG	155
25	(2) INFORMATION FOR SEQ ID NO: 4912:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 69 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:	
35	CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT	60
	AGCCGTCGA	69
	(2) INFORMATION FOR SEQ ID NO: 4913:	
40 45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 69 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:	
50	TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAAACTG CCTGGCAACG TTCTACTCTA	60
	GCGGAACGT	69

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 69 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:	
	CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA	60
	ATACTTCAT	69
15	(2) INFORMATION FOR SEQ ID NO: 4915:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 70 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:	
25	TATTTCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT	60
	CATCCGCTCA	70
30	(2) INFORMATION FOR SEQ ID NO: 4916:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 base pairs	
35	<ul><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:	
40	TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC	60
	CCTTCCG	67
	(2) INFORMATION FOR SEQ ID NO: 4917:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 161 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:	

	TCCACCGTTG ACTAAGGTTC CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA	120
	GGCGCACGTA GGCGATGATA CAGGTTATAT CCTNACACCT A	161
5	(2) INFORMATION FOR SEQ ID NO: 4918:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 68 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:	
	GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC	60
	ACATATGT	68
20	(2) INFORMATION FOR SEQ ID NO: 4919:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919: GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG	60
	AGTGACAATA CTTCAGGG	78
35	(2) INFORMATION FOR SEQ ID NO: 4920:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 68 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:	
45	AATTTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTCG	60
	TACTTCGC	68
50	(2) INFORMATION FOR SEQ ID NO: 4921:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 67 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:	
5	AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC	60
3	TTTACTG	67
	(2) INFORMATION FOR SEQ ID NO: 4922:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 66 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:	
	GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT	60
20	GTCATG	66
	(2) INFORMATION FOR SEQ ID NO: 4923:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 73 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:	
	GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA	60
35	TCGTGGGTGG GAG	73
	(2) INFORMATION FOR SEQ ID NO: 4924:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 89 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:	
	GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC	60
50	TGATGACATA TGCACCGTAA TTCCAAAAA	89
	(2) INFORMATION FOR SEQ ID NO: 4925:	

(A) LENGTH: 68 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:	
10	AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT	60
	ACCTCCAA	68
	(2) INFORMATION FOR SEQ ID NO: 4926:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 73 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:	
25	ACGAAAGGCG TAACGATTTG GGCACTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA	60
25	CCTGTGAAGA TGC	73
	(2) INFORMATION FOR SEQ ID NO: 4927:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 69 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:	
	ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG	60
40	CTCGTTGAG	69
	(2) INFORMATION FOR SEQ ID NO: 4928:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 70 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:	
	AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC	60
55		

	(2) INFORMATION FOR SEQ ID NO: 4929:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 83 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:	
	GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG	60
15	GTGGGTCCCG ACACAGAGAA ATT	83
	(2) INFORMATION FOR SEQ ID NO: 4930:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 66 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930: CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT	60
	ACTCTA	66
30	(2) INFORMATION FOR SEQ ID NO: 4931:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:	
	AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA	60
	GACCG	65
45	(2) INFORMATION FOR SEQ ID NO: 4932:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 73 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA	60
_	CACCAGTGGG CGA	73
5	(2) INFORMATION FOR SEQ ID NO: 4933:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:	
	TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT	60
	GTCTG	65
20	(2) INFORMATION FOR SEQ ID NO: 4934:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 120 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:  GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCTT	60
	TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG	120
	(2) INFORMATION FOR SEQ ID NO: 4935:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 72 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:	
45	GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT	60
	GGATAACGGT TG	72
50	(2) INFORMATION FOR SEQ ID NO: 4936:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 64 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:	
5	CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT	60
J	CTGC	64
	(2) INFORMATION FOR SEQ ID NO: 4937:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 64 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:	
	ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT	60
20	TGGT	64
	(2) INFORMATION FOR SEQ ID NO: 4938:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 63 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:	
	CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA	60
35	GAT	63
	(2) INFORMATION FOR SEQ ID NO: 4939:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 63 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:	
	TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT	60
50	CCT	63
50	(2) INFORMATION FOR SEQ ID NO: 4940:	

	<ul><li>(A) LENGTH: 68 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:	
10	GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT	60
, 0	TAGCTCAG	68
	(2) INFORMATION FOR SEQ ID NO: 4941:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 62 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:	
	CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG	60
25	CG	62
	(2) INFORMATION FOR SEQ ID NO: 4942:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 89 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:	
	TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG	60
40	TGCAAGTTGG GGTAGGGCCC AACACAGAA	89
	(2) INFORMATION FOR SEQ ID NO: 4943:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 69 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:	
	AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT	60

	(2) INFORMATION FOR SEQ ID NO: 4944:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 77 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:	
	CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT	60
15	GACGAATACG TAATTGA	77
	(2) INFORMATION FOR SEQ ID NO: 4945:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 75 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:	
	GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTTGAAGTT	60
30	CAGGTAACAC TGAAT	75
	(2) INFORMATION FOR SEQ ID NO: 4946:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 135 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:	
	ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT	60
45	TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG	120
	TACAGCGCTG ACACT	135
	(2) INFORMATION FOR SEQ ID NO: 4947:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 61 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:	
	GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTCC TTTCTCTTCC	60
5	т	61
	(2) INFORMATION FOR SEQ ID NO: 4948:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 70 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:	
	GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT	60
20	TGTTTGAATC	70
	(2) INFORMATION FOR SEQ ID NO: 4949:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 66 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:	
	CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC	60
35	CTATTC	66
	(2) INFORMATION FOR SEQ ID NO: 4950:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:	
	GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT	60
50	TCACCGTAGG CATGCTGG	78
	(2) INFORMATION FOR SEQ ID NO: 4951:	
<i>EE</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs	
55		

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:	
	CCGCGATAAT AAAAAATAAT GGCGGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG	60
10	G	61
	(2) INFORMATION FOR SEQ ID NO: 4952:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 68 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:	
	ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC	60
25	TGTAACCA	68
	(2) INFORMATION FOR SEQ ID NO: 4953:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 59 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:	
	ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA	59
40	(2) INFORMATION FOR SEQ ID NO: 4954:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:	
50	CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT	60
	(2) INFORMATION FOR SEQ ID NO: 4955:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:	
	AAGGCGTAAC GATTTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT	59
		29
10	(2) INFORMATION FOR SEQ ID NO: 4956:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:	
20	AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC	59
	(2) INFORMATION FOR SEQ ID NO: 4957:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 77 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:	
	ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	60
35	TTTCAATGTA CAATTTC	77
	(2) INFORMATION FOR SEQ ID NO: 4958:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 59 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:	
	TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA	59
50	(2) INFORMATION FOR SEQ ID NO: 4959:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 59 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:	
5	GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG	59
_	(2) INFORMATION FOR SEQ ID NO: 4960:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:	
	TATTAACTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA	59
20	(2) INFORMATION FOR SEQ ID NO: 4961:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 59 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:	
30	ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA	59
	(2) INFORMATION FOR SEQ ID NO: 4962:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:	
	CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA	59
45	(2) INFORMATION FOR SEQ ID NO: 4963:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) OTRANDEDNESS double	
50	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG	60
_	(2) INFORMATION FOR SEQ ID NO: 4964:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:	
15	TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG	59
	(2) INFORMATION FOR SEQ ID NO: 4965:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:	
	AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG	59
30	(2) INFORMATION FOR SEQ ID NO: 4966:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 59 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:	
40	TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG	59
	(2) INFORMATION FOR SEQ ID NO: 4967:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:	
	CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTGCGCT ATGTATATCG CATTAAACGT	60
55		

	(2) INFORMATION FOR SEQ ID NO: 4968:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:	
	GCCTCCGTTA CTTTTAGAGG CGACGCCCAG TCAAACTGCC CGCTGACACT GTCTCCCACC	60
15	(2) INFORMATION FOR SEQ ID NO: 4969:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:	
	CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG	59
	(2) INFORMATION FOR SEQ ID NO: 4970:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:	
	CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG	60
40	TTACG	65
	(2) INFORMATION FOR SEQ ID NO: 4971:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 100 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:	
	CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT	60
55		

	(2) INFORMATION FOR SEQ ID NO: 4972:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 67 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:	
	AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT	60
15	AGGTAGG	67
	(2) INFORMATION FOR SEQ ID NO: 4973:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:	
	TGTGTACTTA AAAATATGAA TACATGAGTA AAACTCATGC ATAAGAAATA CTAATTTC	58
30	(2) INFORMATION FOR SEQ ID NO: 4974:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 58 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:	
40	ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA	58
	(2) INFORMATION FOR SEQ ID NO: 4975:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 68 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:	
	GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG	60
55		

	(2) INFORMATION FOR SEQ ID NO: 4976:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:	
	TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT	59
15	(2) INFORMATION FOR SEQ ID NO: 4977:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
05	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:	
25	TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT	58
	(2) INFORMATION FOR SEQ ID NO: 4978:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:	
	GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG	58
40	(2) INFORMATION FOR SEQ ID NO: 4979:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:	
	TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC	60
	(2) INFORMATION FOR SEQ ID NO: 4980:	
55		

(A) LENGTH: 58 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:	
10	AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC	58
	(2) INFORMATION FOR SEQ ID NO: 4981:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 75 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:	
	GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA	60
25	AAGATGAATC AAAGT	75
20	(2) INFORMATION FOR SEQ ID NO: 4982:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:	
	GTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA	58
	(2) INFORMATION FOR SEQ ID NO: 4983:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 61 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(b) TOPOLOGI: Timeat	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:	
50	TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG	60
	A	61
	(2) INFORMATION FOR SEQ ID NO: 4984:	
55		

5	(A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:	
10	GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG	60
	GAAA	64
	(2) INFORMATION FOR SEQ ID NO: 4985:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(e) 1010 <b>22</b>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:	
25	CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT	59
	(2) INFORMATION FOR SEQ ID NO: 4986:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 57 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:	
	TGATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT	57
40	(2) INFORMATION FOR SEQ ID NO: 4987:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 57 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
45	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:	
50	AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT	57
	(2) INFORMATION FOR SEQ ID NO: 4988:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 57 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	( ') CDOVENIAL DESCRIPTION OF TO NO. 4000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:	
	TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA	57
10	(2) INFORMATION FOR SEQ ID NO: 4989:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:	
20	TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG	57
	(2) INFORMATION FOR SEQ ID NO: 4990:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 61 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:	
	AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT	60
35	G	61
	(2) INFORMATION FOR SEQ ID NO: 4991:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:	
	TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC	60
50	ACCGA	65
	(2) INFORMATION FOR SEQ ID NO: 4992:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 57 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:	
	GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT	57
10	(2) INFORMATION FOR SEQ ID NO: 4993:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:	
20	CCAATGCGGC TCATCGCATC CATTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG	57
	(2) INFORMATION FOR SEQ ID NO: 4994:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:	
	CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG	57
35	(2) INFORMATION FOR SEQ ID NO: 4995:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 73 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:	
	CAAACTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC	60
	ATGCCGGTCT ACG	73
50	(2) INFORMATION FOR SEQ ID NO: 4996:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 65 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
55	(C) SIMMODDINGS. downer	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:	
5	ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG	60
	TAAGC	65
	(2) INFORMATION FOR SEQ ID NO: 4997:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:	
20	ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT	58
20	(2) INFORMATION FOR SEQ ID NO: 4998:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:	
	AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG	56
	(2) INFORMATION FOR SEQ ID NO: 4999:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:	
45	GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTTG	56
45	(2) INFORMATION FOR SEQ ID NO: 5000:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 56 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: doubte  (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:	
	TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC	56
5	(2) INFORMATION FOR SEQ ID NO: 5001:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:	
	GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC	56
	(2) INFORMATION FOR SEQ ID NO: 5002:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 56 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:	
30	CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG	56
	(2) INFORMATION FOR SEQ ID NO: 5003:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:	
	TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA	56
45	(2) INFORMATION FOR SEQ ID NO: 5004:	•
50	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 57 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
<i>55</i>	(D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:	

	(2) INFORMATION FOR SEQ ID NO: 5005:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:	
	GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCACTAGAA GCCGATG	57
15	(2) INFORMATION FOR SEQ ID NO: 5006:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:	
	GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG	57
	(2) INFORMATION FOR SEQ ID NO: 5007:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 69 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:	
40	CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA	60
40	AACCAAAGA	69
	(2) INFORMATION FOR SEQ ID NO: 5008:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:	
55	AAAAGCTTGT TACAAGCGCT ATTTTCGTTC AGTCAACTAC TGCCAATATA ACTTCGT	57

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:	
	ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC	56
	(2) INFORMATION FOR SEQ ID NO: 5010:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(2) Totoboot. Timeat	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:	
25	GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC	60
23	TTGGG	65
	(2) INFORMATION FOR SEQ ID NO: 5011:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 56 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35	10, 20000001, 2000000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:	
40	TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA	56
	(2) INFORMATION FOR SEQ ID NO: 5012:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:	
	CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTTGATAA ACAGTCGCTT	60
	(2) INFORMATION FOR SEQ ID NO: 5013:	00
55	12) INICIDINIZION FOR SEQ ID NO. SUIS:	

	<ul><li>(A) LENGTH: 63 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:	
10	GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC	60
	ACA	63
	(2) INFORMATION FOR SEQ ID NO: 5014:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(D) TOPOLOGI: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:	
25	TAGGGTAGTA TCCCACCAGT GGCCTCCACG TAAGCTAGCG CTTCACGTTT CAAAGGCT	58
	(2) INFORMATION FOR SEQ ID NO: 5015:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 105 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:	
	CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTCGAA	60
40	GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA	105
,,,	(2) INFORMATION FOR SEQ ID NO: 5016:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:	
	CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT	56
55	(2) INFORMATION FOR SEQ ID NO: 5017:	

5	<ul><li>(A) LENGTH: 65 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:	
10	TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT	60
	TATTG	65
	(2) INFORMATION FOR SEQ ID NO: 5018:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 56 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:	
25	GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC	56
	(2) INFORMATION FOR SEQ ID NO: 5019:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35	(wi) CROUDINGS SECONDATION ON TO TO MO FOLD	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:	
	CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC	55
40	(2) INFORMATION FOR SEQ ID NO: 5020:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 58 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
45	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:	
50	TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT	E0
		58
	(2) INFORMATION FOR SEQ ID NO: 5021:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:	
	TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA	55
	(2) INFORMATION FOR SEQ ID NO: 5022:	-
10		
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:	
	AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG	55
	(2) INFORMATION FOR SEQ ID NO: 5023:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 58 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:	
	CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC	58
35	(2) INFORMATION FOR SEQ ID NO: 5024:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:	
45		
	TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT	55
50	(2) INFORMATION FOR SEQ ID NO: 5025:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 63 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55	10, 200000000000000000000000000000000000	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:	
	TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT	60
5	CCA	63
	(2) INFORMATION FOR SEQ ID NO: 5026:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 64 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:	
	GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT	60
20	AACG	64
	(2) INFORMATION FOR SEQ ID NO: 5027:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:	
	AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA	56
35	(2) INFORMATION FOR SEQ ID NO: 5028:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 55 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
40	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:	
	GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT	55
	(2) INFORMATION FOR SEQ ID NO: 5029:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:	
	CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC	54
5	(2) INFORMATION FOR SEQ ID NO: 5030:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:	
	ATCCCCGGGG CCCCAACACA GAGAATTTCG AAAAGAAATT CTACAGGCAA TGCAAGT	57
	(2) INFORMATION FOR SEQ ID NO: 5031:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(with appropriately and ID No. 5031)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:	54
30	TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC	34
	(2) INFORMATION FOR SEQ ID NO: 5032:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:	
	TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA	54
45	(2) INFORMATION FOR SEQ ID NO: 5033:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:	

55

	(2) INFORMATION FOR SEQ ID NO: 5034:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:	
	TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC	54
15	(2) INFORMATION FOR SEQ ID NO: 5035:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:	
	CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA	54
	(2) INFORMATION FOR SEQ ID NO: 5036:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:	
	CTACCATCGA CGCTAAGAGC TTAACTTCTG TGTTCGGCAT GGGAACAGGT GTGA	54
40	(2) INFORMATION FOR SEQ ID NO: 5037:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:	
	CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG	56
55	(2) INFORMATION FOR SEQ ID NO: 5038:	

5	<ul><li>(A) LENGTH: 54 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:	
10	GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT	54
	(2) INFORMATION FOR SEQ ID NO: 5039:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:	
	TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG	54
25	(2) INFORMATION FOR SEQ ID NO: 5040:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 105 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:	
35	TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCNA TGGGAACCAG	60
	CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG	105
40	(2) INFORMATION FOR SEQ ID NO: 5041:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs  (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:	
50	GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC	54
	(2) INFORMATION FOR SEQ ID NO: 5042:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:	
	ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG	54
10	(2) INFORMATION FOR SEQ ID NO: 5043:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:	
20	CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA	53
	(2) INFORMATION FOR SEQ ID NO: 5044:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:	
	ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT	59
35	(2) INFORMATION FOR SEQ ID NO: 5045:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 62 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:	
	TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG	60
	TT	62
50	(2) INFORMATION FOR SEQ ID NO: 5046:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs	
55	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:	
5	CGTCATCCCC ACCTTCCTCC GGTTTGTCAC CGGCAGTCAA CTTAGAGTGC CCA	53
	(2) INFORMATION FOR SEQ ID NO: 5047:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:	
	TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG	53
20	(2) INFORMATION FOR SEQ ID NO: 5048:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 53 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:	
30	CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA	53
	(2) INFORMATION FOR SEQ ID NO: 5049:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:	
	AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT	59
45	(2) INFORMATION FOR SEQ ID NO: 5050:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 111 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
50	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG	60
	TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G	111
5	(2) INFORMATION FOR SEQ ID NO: 5051:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:	
	ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT	53
	(2) INFORMATION FOR SEQ ID NO: 5052:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:	
	CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA	53
30	(2) INFORMATION FOR SEQ ID NO: 5053:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:	
	TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG	53
	(2) INFORMATION FOR SEQ ID NO: 5054:	
<i>45 50</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:	

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	(2) INFORMATION FOR SEQ ID NO: 5055:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:	
	TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG	53
15	(2) INFORMATION FOR SEQ ID NO: 5056:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 63 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:	
25	ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT	60
	CAA	63
30	(2) INFORMATION FOR SEQ ID NO: 5057:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 54 base pairs	
35	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:	
40	CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC	54
	(2) INFORMATION FOR SEQ ID NO: 5058:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:	
	CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG	53

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5	(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 59 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:	
	TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA	59
	(2) INFORMATION FOR SEQ ID NO: 5060:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:	
	AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT	53
25	(2) INFORMATION FOR SEQ ID NO: 5061:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:	
	TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC	55
	(2) INFORMATION FOR SEQ ID NO: 5062:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:	
50	TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA	52
	(2) INFORMATION FOR SEQ ID NO: 5063:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs	
55	•	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:	
	TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA	52
10	(2) INFORMATION FOR SEQ ID NO: 5064:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 76 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:	
20	CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAACT	60
	TTGGAGCGCC TCCGTT	76
25	(2) INFORMATION FOR SEQ ID NO: 5065:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:  CCACCGCTTG TGCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT	54
40	(2) INFORMATION FOR SEQ ID NO: 5066:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:	
	TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG	55
50	(2) INFORMATION FOR SEQ ID NO: 5067:	
55	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:	
5	GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA	52
	(2) INFORMATION FOR SEQ ID NO: 5068:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 82 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:	
	CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA	60
	GCGAGCGGAA ACAACAA CG	82
20	(2) INFORMATION FOR SEQ ID NO: 5069:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:	
	TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA	52
35	(2) INFORMATION FOR SEQ ID NO: 5070:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:	
45	CGACTCGAAG ACTCAATGTC TTCTCCCCAT CACAGCTCAG CCTTAACGAG TA	52
	(2) INFORMATION FOR SEQ ID NO: 5071:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:	
	GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA	52
5	(2) INFORMATION FOR SEQ ID NO: 5072:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:	
	CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA	53
	(2) INFORMATION FOR SEQ ID NO: 5073:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:	
	GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA	52
30	(2) INFORMATION FOR SEQ ID NO: 5074:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:	
	TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCGTAAT AGCTCACTAG TCGC	54
	(2) INFORMATION FOR SEQ ID NO: 5075:	
<b>45</b>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 74 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:	

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	AAACTTCCCT TTGG	74
	(2) INFORMATION FOR SEQ ID NO: 5076:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 53 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:	
15	TGAGCTAATC AGACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAA GAT	53
	(2) INFORMATION FOR SEQ ID NO: 5077:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:  GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA	52
	(2) INFORMATION FOR SEQ ID NO: 5078:	52
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:	
40	GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA AC	52
	(2) INFORMATION FOR SEQ ID NO: 5079:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:	
	ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAATA AT	52

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5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:  AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG	52
	(2) INFORMATION FOR SEQ ID NO: 5081:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:	
25	CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA	52
25	(2) INFORMATION FOR SEQ ID NO: 5082:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:	
	CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA	56
40	(2) INFORMATION FOR SEQ ID NO: 5083:  (i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	<b>\-,</b>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:	
50	AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCCTA	60
	CG	62
	(2) INFORMATION FOR SEQ ID NO: 5084:	
55		

5	<ul><li>(A) LENGTH: 52 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:	
10	GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG	52
	(2) INFORMATION FOR SEQ ID NO: 5085:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 78 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:	
	TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC	60
	CCGAGGAGCG GATTAACA	78
25	(2) INFORMATION FOR SEQ ID NO: 5086:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:	
	ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT	52
	(2) INFORMATION FOR SEQ ID NO: 5087:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(5) 20100021 221000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:	
50	AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G	51
	(2) INFORMATION FOR SEQ ID NO: 5088:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 51 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:	
	AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T	51
		31
10	(2) INFORMATION FOR SEQ ID NO: 5089:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 51 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	10/ 00000000000000000000000000000000000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:	
20	AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G	51
	(2) INFORMATION FOR SEQ ID NO: 5090:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:	
	CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC C	51
35	(2) INFORMATION FOR SEQ ID NO: 5091:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> </ul>	
40	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:	
	CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T	51
	(2) INFORMATION FOR SEQ ID NO: 5092:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
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	(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:	
	TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA	55
5	(2) INFORMATION FOR SEQ ID NO: 5093:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:	
	CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A	51
	(2) INFORMATION FOR SEQ ID NO: 5094:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:	
00	ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A	51
30	(2) INFORMATION FOR SEQ ID NO: 5095:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 77 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:	
	AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT	60
	ATTGTGCCAC CGATTGA	77
45	(2) INFORMATION FOR SEQ ID NO: 5096:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

	TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG	52
	(2) INFORMATION FOR SEQ ID NO: 5097:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:	
15	GGGTCTGTTT TCTAATTTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A	51
	(2) INFORMATION FOR SEQ ID NO: 5098:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:	
		51
	CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T	21
30	(2) INFORMATION FOR SEQ ID NO: 5099:  (i) SEQUENCE CHARACTERISTICS:	
35	<ul><li>(A) LENGTH: 51 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:	
40	CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A	51
	(2) INFORMATION FOR SEQ ID NO: 5100:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	( 1)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:	
	GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A	51
55		

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 64 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:	
	TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA	60
	CACA	64
15	(2) INFORMATION FOR SEQ ID NO: 5102:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 58 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:	
25	TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG	58
	(2) INFORMATION FOR SEQ ID NO: 5103:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:	
	ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT	50
40	(2) INFORMATION FOR SEQ ID NO: 5104:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 53 base pairs  (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:	
	GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT	53
	(2) INFORMATION FOR SEQ ID NO: 5105:	
55		

	<ul><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:	
10	ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT	50
	(2) INFORMATION FOR SEQ ID NO: 5106:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:	
	TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA	50
25	(2) INFORMATION FOR SEQ ID NO: 5107:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:	
35	TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT	50
	(2) INFORMATION FOR SEQ ID NO: 5108:	
40	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:	
	CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA	50
50	(2) INFORMATION FOR SEQ ID NO: 5109:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: double	

	(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:	
5	AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT	50
3	(2) INFORMATION FOR SEQ ID NO: 5110:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:	
	ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA	53
	(2) INFORMATION FOR SEQ ID NO: 5111:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 53 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:	
30	CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC	53
	(2) INFORMATION FOR SEQ ID NO: 5112:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:	
	GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT	50
45	(2) INFORMATION FOR SEQ ID NO: 5113:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
50	(D) TOPOLOGY: linear	

	AGANTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG	50
	(2) INFORMATION FOR SEQ ID NO: 5114:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:	
15	GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG	50
	(2) INFORMATION FOR SEQ ID NO: 5115:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:	
	CTTGATTAAC TCATTATCAA GTTATGCACG TGTAAATGAA TTCGGCTTTA TCGAA	55
30	(2) INFORMATION FOR SEQ ID NO: 5116:  (i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:	
40	GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA	50
	(2) INFORMATION FOR SEQ ID NO: 5117:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:	
	CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn	50
	CUANUICUAN INACAUCICA GUNICADATA CIGARAN	

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:	
	CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA	50
	(2) INFORMATION FOR SEQ ID NO: 5119:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:	
	AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA	60
25	(2) INFORMATION FOR SEQ ID NO: 5120:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:	
	CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG	50
	(2) INFORMATION FOR SEQ ID NO: 5121:	
40	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 61 base pairs</li></ul>	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:	
	ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG	60
50	T	61
	(2) INFORMATION FOR SEQ ID NO: 5122:	
55		

5	<ul><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:	
10	TAGCGACTCA GATTCAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA	50
	(2) INFORMATION FOR SEQ ID NO: 5123:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:	
	TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT	50
25	(2) INFORMATION FOR SEQ ID NO: 5124:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:	
35	CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCGAGAAG GTCTCTATCT	60
	(2) INFORMATION FOR SEQ ID NO: 5125:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 64 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:	
	AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT	60
50	AGAA	64
	(2) INFORMATION FOR SEQ ID NO: 5126:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 57 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:	
	GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT	57
10	(2) INFORMATION FOR SEQ ID NO: 5127:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:	
20	GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG	50
	(2) INFORMATION FOR SEQ ID NO: 5128:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:	
	GCCGATTTTA GCAGTTGTTG CTTCGTTCAA TTTTATGGGG CCATTTATGG	50
35	(2) INFORMATION FOR SEQ ID NO: 5129:	
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:	
45	TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A	51
	(2) INFORMATION FOR SEQ ID NO: 5130:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:	
5	CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT	57
-	(2) INFORMATION FOR SEQ ID NO: 5131:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:	
	TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A	51
20	(2) INFORMATION FOR SEQ ID NO: 5132:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 51 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:	
30	TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A	51
	(2) INFORMATION FOR SEQ ID NO: 5133:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:	
	ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC	59
45	(2) INFORMATION FOR SEQ ID NO: 5134:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
50	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:	

	(2) INFORMATION FOR SEQ ID NO: 5135:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:	
	CAATACNAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG	50
15	(2) INFORMATION FOR SEQ ID NO: 5136:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:	
25	GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC	52
	(2) INFORMATION FOR SEQ ID NO: 5137:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:	
	TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT	50
40	(2) INFORMATION FOR SEQ ID NO: 5138:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:	
	CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT ANAGCTCCAC	50
	(2) INFORMATION FOR SEQ ID NO: 5139:	
55		

5	<ul><li>(A) LENGTH: 52 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:	
10	GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC	52
	(2) INFORMATION FOR SEQ ID NO: 5140:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:	
	GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT	56
25	(2) INFORMATION FOR SEQ ID NO: 5141:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:	
35	AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA	52
	(2) INFORMATION FOR SEQ ID NO: 5142:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 56 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:	
	CACGCTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT	56
50	(2) INFORMATION FOR SEQ ID NO: 5143:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 75 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
55	(C) STRANDEDNESS: double	

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 53 base pairs  (B) TYPE: nucleic acid		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:	
CGCCATTGCG AAGAT  (2) INFORMATION FOR SEQ ID NO: 5144:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:  GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT  20 (2) INFORMATION FOR SEQ ID NO: 5145: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	-	CTCCTAAAAC AATTTACATC CAAACCTTCA TCACTCAC	60
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:  GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT  (2) INFORMATION FOR SEQ ID NO: 5145:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  51  (2) INFORMATION FOR SEQ ID NO: 5147: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	5	CGCCATTGCG AAGAT	75
(A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:  GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55  (2) INFORMATION FOR SEQ ID NO: 5145:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCCGT T 51  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(2) INFORMATION FOR SEQ ID NO: 5144:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:  GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT  20 (2) INFORMATION FOR SEQ ID NO: 5145:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	10	<ul><li>(A) LENGTH: 55 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT  (2) INFORMATION FOR SEQ ID NO: 5145:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	15		
(2) INFORMATION FOR SEQ ID NO: 5145:  (i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (C) STRANDEDNESS: double		GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT	55
(A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:  GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	20	(2) INFORMATION FOR SEQ ID NO: 5145:	
GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG  (2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS:	25	<ul><li>(A) LENGTH: 53 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
(2) INFORMATION FOR SEQ ID NO: 5146:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	30		5.3
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double			53
(A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  40  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  45  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:  AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  45  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	35	<ul><li>(A) LENGTH: 51 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T  45  (2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	40		
(2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:	
(2) INFORMATION FOR SEQ ID NO: 5147:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double		AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T	51
(A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	45	(2) INFORMATION FOR SEQ ID NO: 5147:	
	50	<ul><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:	
	CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA	50
5	(2) INFORMATION FOR SEQ ID NO: 5148:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:	
	GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA	60
	(2) INFORMATION FOR SEQ ID NO: 5149:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(b) 10101001. 11Md1	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:	
	AAAGCACACC CGGAAAACTG AAACATCTTA AGTACCCGGA GnAAGAGAAA	50
30	(2) INFORMATION FOR SEQ ID NO: 5150:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:	
	GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG	56
	(2) INFORMATION FOR SEQ ID NO: 5151:	
<i>45 50</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 56 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:	

	(2) INFORMATION FOR SEQ ID NO: 5152:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 59 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:	
	CTATTCTCTG TGTCGGGCTC ACCCCAACTT GCACACTATT GTAAGCTGAC TTTCCTCCA	59
15	(2) INFORMATION FOR SEQ ID NO: 5153:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 65 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:	
25	TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA	60
	ATACA	65
30	(2) INFORMATION FOR SEQ ID NO: 5154:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 91 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:	
40	CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC	60
	TCCGTGCCAG CCGCCGCGT ACTACGTGGT G	91
	(2) INFORMATION FOR SEQ ID NO: 5155:	
<i>45 50</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 52 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:	

	(2) INFORMATION FOR SEQ ID NO: 5156:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 58 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:	
	GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC	58
15	(2) INFORMATION FOR SEQ ID NO: 5157:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 51 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:	
25	TTGTAACTCC GGTATAGGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT G	51
	(2) INFORMATION FOR SEQ ID NO: 5158:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:	
	TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC	50
40	(2) INFORMATION FOR SEQ ID NO: 5159:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159: TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T	51
	(2) INFORMATION FOR SEQ ID NO: 5160:	
5 <b>5</b>		

(A) LENGTH: 61 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:	
10	AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT	60
	T	61
	(2) INFORMATION FOR SEQ ID NO: 5161:	
15 20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 51 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:	
25	AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T	51
	(2) INFORMATION FOR SEQ ID NO: 5162:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:	
	CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT	55
40	(2) INFORMATION FOR SEQ ID NO: 5163:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 81 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:	
50	CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT	60
	CGTAGTATAA GATTCCGTGT A	81
55	(2) INFORMATION FOR SEQ ID NO: 5164:	

5	<ul><li>(A) LENGTH: 62 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:	
10	GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC	60
	AG	62
	(2) INFORMATION FOR SEQ ID NO: 5165:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:	
25	CAGGGGTCTT TCGTCCTGTG TGGGTAACTG CATCTTCACA GGTACTATGA TTTCA	55
	(2) INFORMATION FOR SEQ ID NO: 5166:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 62 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:	
	AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT	60
	AA	62
40	(2) INFORMATION FOR SEQ ID NO: 5167:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:	
	CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG	52
	(2) INFORMATION FOR SEQ ID NO: 5168:	
EE		

5	<ul><li>(A) LENGTH: 56 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:	
10	TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAAACTAG ATAAGTAGTA AATATA	56
	(2) INFORMATION FOR SEQ ID NO: 5169:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:	
	CTTGGACGTC GGTGGGTAGT CGAAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA	55
25	(2) INFORMATION FOR SEQ ID NO: 5170:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:	
55	CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA	52
	(2) INFORMATION FOR SEQ ID NO: 5171:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:	
	GGGCTTnGGA CATTAAGTTC TNAGGCAATG TAAAAAAGCT GATTTCTATT	50
50	(2) INFORMATION FOR SEQ ID NO: 5172:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 60 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
55	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:	
5	AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG	60
5	(2) INFORMATION FOR SEQ ID NO: 5173:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:	
	GTTTTATTTT TTTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn	50
20	(2) INFORMATION FOR SEQ ID NO: 5174:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 57 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:	
30	CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAACTT CGGAGTAGGT CTCTTTA	57
	(2) INFORMATION FOR SEQ ID NO: 5175:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:	
	GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA	60
45	(2) INFORMATION FOR SEQ ID NO: 5176:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 50 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
50	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTCATA	50
	(2) INFORMATION FOR SEQ ID NO: 5177:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(5) Totoboot. Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:	
15	AGTTACGTTC TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG	50
	(2) INFORMATION FOR SEQ ID NO: 5178:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 53 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:	
	GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG	53
	(2) INFORMATION FOR SEQ ID NO: 5179:	
<i>30 35</i>	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 83 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:	
40	CGGTAACTTC ATACCTTTTA ACATATTTTG CATTTGATTG CGTTTACCTT TTTTACCTTT	60
	ACCGCCACCA GTGAACTGTT TCA	83
	(2) INFORMATION FOR SEQ ID NO: 5180:	
45 50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 66 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:	

	TTTAAA	66
	(2) INFORMATION FOR SEQ ID NO: 5181:	
5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 67 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:	
15	GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC	60
	GCAATAT	67
	(2) INFORMATION FOR SEQ ID NO: 5182:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 55 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:	
	TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT	55
30	(2) INFORMATION FOR SEQ ID NO: 5183:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:	
	GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGNAC GAACACCAAT	50
	(2) INFORMATION FOR SEQ ID NO: 5184:	
45 50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 62 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:	

	CC	62
	(2) INFORMATION FOR SEQ ID NO: 5185:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 55 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:	
15	GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT	55
	(2) INFORMATION FOR SEQ ID NO: 5186:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:	
	CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG	50
30	(2) INFORMATION FOR SEQ ID NO: 5187:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs	
35	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:	
40	TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC	50
	(2) INFORMATION FOR SEQ ID NO: 5188:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:	
55	AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTNAGTC GCTANNCCAG	50
55		

5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 54 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:	
70	ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT	54
	(2) INFORMATION FOR SEQ ID NO: 5190:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 50 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:	
	CTTTAATGGG CGAACAGNAC CCTTGGACCG ACTACAGCCC AGATCGATGA	50
25	(2) INFORMATION FOR SEQ ID NO: 5191:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:	
	ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT	60
40	(2) INFORMATION FOR SEQ ID NO:5192:  (i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 320 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5192:	
	Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu	
55	1 5 10 15	

5	Leu	Ile	Ser 35	Ser	Lys	Ala	Gly	Asp 40	Val	Thr	Val	Ala	Asp 45	Thr	Met	Lys
	Lys	Ile 50	Gly	Lys	Asp	Gln	Ile 55	Ala	Asn	Ala	Ser	Phe 60	Thr	Glu	Met	Leu
10	Asn 65	Lys	Ile	Leu	Ala	Asp 70	Lys	Tyr	Lys	Asn	Lys 75	Val	Asn	Asp	Lys	Lys 80
	Ile	Asp	Glu	Gln	Ile 85	Glu	Lys	Met	Gln	Lys 90	Gln	Tyr	Gly	Gly	Lys 95	Asp
15	Lys	Phe	Glu	Lys 100	Ala	Leu	Gln	Gln	Gln 105	Gly	Leu	Thr	Ala	Asp 110	Lys	Tyr
	Lys	Glu	<b>As</b> n 115	Leu	Arg	Thr	Ala	Ala 120	Tyr	His	Lys	Glu	Leu 125	Leu	Ser	Asp
20	Lys	Ile 130	Lys	Ile	Ser	Asp	Ser 135	Glu	Ile	Lys	Glu	Asp 140	Ser	Lys	Lys	Ala
25	Ser 145	His	Ile	Leu	Ile	<b>Lys</b> 150	Val	Lys	Ser	Lys	Lys 155	Ser	Asp	Xaa	Glu	Gly 160
	Leu	Asp	Asp	Lys	Glu 165	Ala	Lys	Gln	Lys	Ala 170	Glu	Glu	Ile	Gln	Lys 175	Glu
30	Val	Ser	Lys	<b>Asp</b> 180	Pro	Ser	Lys	Phe	Gly 185	Glu	Ile	Ala	Lys	Lys 190	Glu	Ser
	Met	Asp	Thr 195	Gly	Ser	Ala	Lys	Lys 200	Asp	Gly	Glu	Leu	Gly 205	Tyr	Val	Leu
35	Lys	Gly 210	Gln	Thr	Asp	Lys	Asp 215	Phe	Glu	Lys	Ala	Leu 220	Phe	Lys	Leu	Lys
	Asp 225	Gly	Glu	Val	Ser	Glu 230	Val	Val	Lys	Ser	Ser 235	Phe	Gly	Tyr	His	Ile 240
40	Ile	Lys	Ala	Asp	Lys 245	Pro	Thr	Asp		<b>As</b> n 250		Glu	Lys	Gln	Ser 255	Leu
45	Lys	Glu	Lys	<b>Le</b> u 260	Val	Asp	Gln	Lys	Val 265	Gln	Lys	Asn	Pro	Lys 270	Leu	Leu
	Thr	Asp	Ala 275	Tyr	Lys	Asp	Leu	Leu 280	Lys	Glu	Tyr	Asp	Val 285	Asp	Phe	Lys
50	Asp	Arg 290	Asp	Ile	Lys	Ser	Val 295	Val	Glu	Asp	Lys	Ile 300	Leu	Asn	Pro	Glu
	Lys 305	Leu	Lys	Gln	Gly	Gly 310	Ala	Gln	Gly	Gly	Gln 315	Ser	Gly	Met	Ser	Gln 320
55	 															

(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

5		(D)	TOI	POLOG	SY: ]	inea	ir									
	(ii)	MOLE	ECULI	TYP	PE: p	rote	ein									
10	(xi)	SEQU	JENCI	E DES	SCRII	PTION	1: SI	EQ II	O NO	:5193	3:					
	Met 1	Asn	Lys	Val	Ile 5	Lys	Met	Leu	Val	Val 10	Thr	Leu	Ala	Phe	Leu 15	Leu
15	Val	Leu	Ala	Gly 20	Cys	Ser	Gly	Asn	Ser 25	Asn	Lys	Gln	Ser	Ser 30	Asp	Asn
20	Lys	Asp	Lys 35	Glu	Thr	Thr	Ser	Ile 40	Lys	His	Ala	Met	Gly 45	Thr	Thr	Glu
	Ile	Lys 50	Gly	Lys	Pro	Lys	Arg 55	Val	Val	Thr	Leu	Tyr 60	Gln	Gly	Ala	Thr
25	Asp 65	Val	Ala	Val	Ser	Leu 70	Gly	Val	Lys	Pro	Val 75	Gly	Ala	Val	Glu	Ser 80
	Trp	Thr	Gln	Lys	Pro 85	Lys	Phe	Glu	Tyr	Ile 90	Lys	Asn	Asp	Leu	Lys 95	Asp
30	Thr	Lys	Ile	<b>Val</b> 100	Gly	Gln	Glu	Pro	<b>Ala</b> 105	Pro	Asn	Leu	Glu	Glu 110	Ile	Ser
	Lys	Leu	Lys 115	Pro	Asp	Leu	Ile	Val 120	Ala	Ser	Lys	Val	Arg 125	Asn	Glu	Lys
35	Val	Tyr 130	Asp	Gln	Leu	Ser	Lys 135	Ile	Ala	Pro	Thr	Val 140	Ser	Thr	Asp	Thr
	<b>Val</b> 145	Phe	Lys	Phe	Lys	<b>Asp</b> 150	Thr	Thr	Lys	Leu	Met 155	Gly	Lys	Ala	Leu	Gly 160
40	Lys	Glu	Lys	Glu	Ala 165	Glu	Asp	Leu	Leu	Lys 170	Lys	Tyr	Asp	Asp	Lys 175	Val
45	Ala	Ala	Phe	Gln 180	Lys	Asp	Ala	Lys	Ala 185	Lys	Tyr	Lys	Asp	Ala 190	Trp	Pro
	Leu	Lys	Ala 195	Ser	Val	Val	Asn	Phe 200	Arg	Ala	Asp	His	Thr 205	Arg	Ile	Tyr
50	Ala	Gly 210	Gly	Tyr	Ala	Gly	Glu 215	Ile	Leu	Asn	Asp	Leu 220	Gly	Phe	Lys	Arg
	Asn 225	Lys	Asp	Leu	Gln	Lys 230	Gln	Val	Asp	Asn	Gly 235	Lys	Asp	Ile	Ile	Gln 240
55	Leu	Thr	Ser	Lys	Glu 245	Ser	Ile	Pro	Leu	Met 250		Ala	Asp	His	Ile 255	Phe

	Val	Val	Lys	Ser 260	Asp	Pro	Asn	Ala	Lys 265	Asp	Ala	Ala	Leu	Val 270	Lys	Lys
5	Thr	Glu	Ser 275	Glu	Trp	Thr	Ser	Ser 280	Lys	Glu	Trp	Lys	Asn 285	Leu	Asp	Ala
	Val	Lys 290	Asn	Asn	Gln	Val	Ser 295	Asp	Asp	Leu	Asp	Glu 300	Ile	Thr	Trp	Asn
10	<b>Leu</b> 305	Ala	Gly	Gly	Tyr	Lys 310	Ser	Ser	Leu	Lys	Leu 315	Ile	Asp	Asp	Leu	Tyr 320
15	Glu	Lys	Leu	Asn	Ile 325	Glu	Lys	Gln	Ser	Lys 330						
15	(2) INFO	RMAT 1	ON I	FOR S	SEQ 1	D NO	):519	94:								
20	(i)	(B)	LEN TYPE	NGTH: PE: 8 RANDI	ARACT : 314 amino EDNES GY: ]	ami aci	ino a id singl	acids	5							
25	(ii)	MOLE	ECULI	E TYI	PE: p	prote	in									
	(xi)	SEQU	JENCI	E DES	SCRIE	PTION	1: SI	EQ II	NO:	5194	<b>!</b> :					
30	Met 1	Thr	Arg	Lys	Phe 5	Arg	Thr	Leu	Ile	Leu 10	Ile	Leu	Ile	Ala	Thr 15	Ile
	Ala	Leu	Ser	Gly 20	Cys	Ala	Asn	Asp	Asp 25	Gly	Ile	Tyr	Ser	Asp 30	Lys	Gly
35	Gln	Val	Phe 35	Arg	Lys	Ile	Leu	Ser 40	Ser	Asp	Leu	Thr	Ser 45	Leu	Asp	Thr
40	Ser	Leu 50	Ile	Thr	Asp	Glu	Ile 55	Ser	Ser	Glu	Val	Thr 60	Ala	Gln.	Thr	Phe
40	Glu 65	Gly	Leu	Tyr	Thr	Leu 70	Gly	Lys	Gly	Asp	Lys 75	Pro	Val	Leu	Gly	Val 80
<b>45</b>	Ala	Lys	Ala	Phe	Pro 85	Glu	Lys	Ser	Lys	Asp 90	Gly	Lys	Thr	Leu	Lys 95	Val
	Lys	Leu	Arg	Ser 100	Asp	Ala	Lys	Trp	Ser 105	Asn	Gly	Asp	Lys	<b>Val</b> 110	Thr	Ala
50	Gln	Asp	Phe 115	Val	Tyr	Ala	Trp	Arg 120	Lys	Thr	Val	Asp	Pro 125	Lys	Thr	Gly
	Ser	Glu 130	Phe	Ala	Tyr	Ile	Met 135	Gly	Asp	Ile	ГÅа	Asn 140	Ala	Ser	Asp	Ile
55	Ser 145	Thr	Gly	Lys	Lys	Pro 150	Val	Glu	Gln	Leu	Gly 155	Ile	ГЛа	Ala	Leu	Asn 160

		Asp	Glu	Thr	Leu	Gln 165	Ile	Glu	Leu	Glu	Lys 170	Pro	Val	Pro	Tyr	Ile 175	Asn
5		Gln	Leu	Leu	Ala 180	Leu	Asn	Thr	Phe	Ala 185	Pro	Gln	Asn	Glu	Lys 190	Val	Ala
		Lys	Lys	Tyr 195	Gly	Lys	Asn	Tyr	Gly 200	Thr	Ala	Ala	Asp	Arg 205	Ala	Val	Tyr
10		Asn	Gly 210	Pro	Phe	Lys	Val	Asp 215	Asp	Trp	Lys	Gln	Glu 220	Asp	Lys	Thr	Leu
		Leu 225	Ser	Lys	Asn	Gln	Tyr 230	Tyr	Trp	<b>As</b> p	Lys	Lys 235	Asn	Val	Lys	Leu	<b>As</b> p 240
15		Lys	Val	Asn	Tyr	Lys 245	Val	Ile	Lys	Asp	<b>Leu</b> 250	Gln	Ala	Gly	Ala	Ser 255	Leu
20		Tyr	Asp	Thr	Glu 260	Ser	Val	Asp	Asp	Ala 265	Phe	Ile	Thr	Ala	Asp 270	Gln	Val
		Asn	Lys	Tyr 275	Lys	Asp	Asn	Lys	Gly 280	Leu	Asn	Phe	Val	Leu 285	Thr	Thr	Gly
25		Thr	Phe 290	Phe	Val	Lys	Met	<b>As</b> n 295	Glu	Lys	Gln	Tyr	Pro 300	Asp	Phe	Lys	Asn
		Lys 305	Asn	Leu	Arg	Leu	<b>Xaa</b> 310	Ser	His	Lys	Gln						
30	(2) INFORMATION FOR SEQ ID NO:5195:																
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 280 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>																
35		(ii)	MOLI														
10																	
40		(xi)	SEQ	JENCI	E DE	SCRI	PTIO	N: S	EQ I	D NO	:519	5 :					
45		Met 1	Lys	Arg	Leu	Ile 5	Gly	Leu	Val	Ile	Val 10	Ala	Leu	Val	Leu	Leu 15	Ala
45		Ala	Cys	Gly	Gly 20	Asn	Asn	Asp	Lys	Lys 25	Val	Thr	Ile	Gly	Val 30	Ala	Ser
50		Asn	Asp	Thr 35	Lys	Ala	Trp	Glu	Lys 40	Val	Lys	Glu	Leu	Ala 45	Lys	Lys	Asp
		Asp	Ile 50	Asp	Val	Glu	Ile	Lys 55	His	Phe	Ser	Asp	Tyr 60	Asn	Leu	Pro	Asn
55		Lys 65	Ala	Leu	Asn	Asp	Gly 70	Asp	Ile	Asp	Met	Asn 75	Ala	Phe	Gln	His	Phe 80

		Ala	Pne	Leu	Asp	Gln 85	Tyr	Lys	Lys	Ala	H18 90	Lys	GIÀ	Thr	Lys	95	Ser
5		Ala	Leu	Ser	Thr 100	Thr	Val	Leu	Ala	Pro 105	Leu	Gly	Ile	Tyr	Ser 110	Asp	Lys
		Ile	Lys	Asp 115	Val	Lys	Lys	Val	Lys 120	Asp	Gly	Ala	Lys	Val 125	Val	Ile	Pro
10		Asn	Asp 130	Val	Ser	Asn	Gln	Ala 135	Arg	Ala	Leu	Lys	Leu 140	Leu	Glu	Ala	Ala
15		Gly 145	Leu	Ile	Lys	Leu	<b>Lys</b> 150	Lys	Asp	Phe	Gly	Leu 155	Ala	Gly	Thr	Val	<b>Lys</b> 160
73		Asp	Ile	Thr	Ser	Asn 165	Pro	Lys	His	Leu	Lys 170	Ile	Thr	Ala	Val	Asp 175	Ala
20		Gln	Gln	Thr	Ala 180	Arg	Ala	Leu	Ser	<b>Asp</b> 185	Val	Asp	Ile	Ala	<b>Val</b> 190	Ile	Asn
		Asn	Gly	Val 195	Ala	Thr	Lys	Ala	Gly 200	Lys	Asp	Pro	Lys	Asn 205	Asp	Pro	Ile
25		Phe	Leu 210	Glu	Lys	Ser	Asn	Ser 215	Asp	Ala	Val	Lys	Pro 220	Tyr	Ile	Asn	Ile
		Val 225	Ala	Val	Asn	Asp	Lys 230	Asp	Leu	Asp	Asn	Lys 235	Thr	Tyr	Ala	Lys	11e 240
30		Val	Glu	Leu	Tyr	His 245	Ser	Lys	Glu	Ala	Gln 250	Lys	Ala	Leu	Gln	Glu 255	Asp
		Val	Lys	Asp	Gly 260	Glu	Lys	Pro	Val	Asn 265	Leu	Ser	Lys	Asp	Glu 270	Ile	Lys
35		Ala	Ile	Glu 275	Thr	Ser	Leu	Ala	Lys 280								
	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID NO	0:519	96 :								
40		(i)	(A) (B) (C)	UENCI LEI TYI STI	NGTH PE: 8 RAND!	: 27: amino EDNE:	am: ac: ss: 4	ino a id sing!	acids	5							
45		(ii)	MOL	ECUL	E TY	PE: ]	prot	ein									
50		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ II	D NO	:519	6 :					
		Met 1	Lys	Lys	Leu	Phe 5	Gly	Leu	Ile	Leu	Val 10	Leu	Thr	Phe	Ala	Val 15	Val
55		Leu	Ala	Ala	Cys 20	Gly	Asn	Gly	Asn	Lys 25	Ser	Gly	Ser	Asp	Asp 30	Lys	Lys

		Ile	Thr	Val 35	Ser	Ala	Ser	Pro	Ala 40	Pro	His	Ala	Glu	Ile 45	Leu	Glu	Lys
5		Ala	Lys 50	Pro	Leu	Leu	Glu	Lys 55	Lys	Gly	Tyr	Glu	Leu 60	Asp	Ile	Lys	Thr
		Ile 65	Asn	Asp	Tyr	Thr	Thr 70	Pro	Asn	Lys	Leu	Leu 75	Asp	Lys	Gly	Glu	Ile 80
10		Asp	Ala	Asn	Tyr	Phe 85	Gln	His	Thr	Pro	Tyr 90	Leu	Asn	Thr	Glu	Lys 95	Lys
		Asp	Lys	Gly	Tyr 100	Lys	Ile	Val	Ser	<b>Ala</b> 105	Gly	Asp	Val	His	Leu 110	Glu	Pro
15		Met	Ala	Val 115	Tyr	Ser	Lys	Lys	Tyr 120	Lys	Ser	Leu	Lys	Glu 125	Leu	Pro	Lys
20		Gly	Ala 130	Thr	Val	Tyr	Val	Ser 135	Asn	Asn	Pro	Ala	Glu 140	Gln	Gly	Arg	Phe
. •		Leu 145	Lys	Phe	Phe	Val	<b>Asp</b> 150	Ala	Gly	Leu	Ile	Lys 155	Ile	Lys	Lys	Gly	<b>Va</b> l 160
25		Lys	Ile	Glu	Asp	Ala 165	Lys	Phe	Ser	Asp	Ile 170	Thr	Glu	Asn	Lys	Lys 175	Asp
		Ile	Lys	Phe	Asn 180	Asn	Lys	Gln	Ser	Ala 185	Glu	Phe	Leu	Pro	Lys 190	Ile	Tyr
30		Gln	Asn	Glu 195	Asp	Ala	Asp	Ala	Val 200	Ile	Ile	Asn	Ser	Asn 205	Phe	Ala	Ile
		Glu	Gln 210	Lys	Leu	Asn	Pro	Lys 215	Lys	Asp	Ser	Ile	Ala 220	Val	Glu	Ser	Ala
35		Lys 225	-	Asn	Pro	Tyr	Ala 230	Asn	Leu	Ile	Ala	Val 235	Lys	Glu	Gly	His	Gln 2 <b>4</b> 0
		Asp	Asp	Lys	Lys	11e 245	Lys	Ala	Leu	Ile	Glu 250	Val	Leu	Gln	Ser	Lys 255	Asp
40		Ile	Gln	Asp	Phe 260	Ile	Asn	Glu	Lys	Tyr 265	Asn	Gly	Ala	Val	Ile 270	Pro	Ala
		Lys															
45	(2)	INFO	RMAT	ION I	FOR :	SEQ	ID N	0:51	97:								
50		(i)	(A (B	) LE	NGTH PE:	ARAC : 31 amin	3 am o ac	ino : id	acid	S							
						EDNE GY:			1e								

(ii) MOLECULE TYPE: protein

	(xi)	SEQ	JENCI	E DES	SCRIE	OITS	N: S	EQ II	ON C	: 5197	7 :					
5	Met 1	Lys	Lys	Ile	Lys 5	Tyr	Ile	Leu	Val	Val 10	Phe	Val	Leu	Ser	Leu 15	Thr
	Val	Leu	Ser	Gly 20	Cys	Ser	Leu	Pro	Gly 25	Leu	Gly	Ser	Lys	Ser 30	Thr	Lys
10	Asn	Asp	<b>Val</b> 35	Lys	Ile	Thr	Ala	Leu 40	Ser	Thr	Ser	Glu	Ser 45	Gln	Ile	Ile
	Ser	His 50	Met	Leu	Arg	Leu	Leu 55	Ile	Glu	His	Asp	Thr 60	His	Gly	Lys	Ile
15	Lys 65	Pro	Thr	Leu	Val	Asn 70	Asn	Leu	Gly	Ser	Ser 75	Thr	Ile	Gln	His	Asn 80
	Ala	Leu	Ile	Asn	Gly 85	Asp	Ala	Asn	Ile	Ser 90	Gly	Val	Arg	Tyr	Asn 95	Gly
20	Thr	Asp	Leu	Thr 100	Gly	Ala	Leu	Lys	Glu 105	Ala	Pro	Ile	Lys	Asn 110	Pro	Lys
25	Lys	Ala	Met 115	Ile	Ala	Thr	Gln	Gln 120	Gly	Phe	Lys	Lys	Lys 125	Phe	Asp	Gln
	Thr	Phe 130	Phe	Asp	Ser	Tyr	Gly 135	Phe	Ala	Asn	Thr	Tyr 140	Ala	Phe	Met	Val
30	Thr 145	Lys	Glu	Thr	Ala	Lys 150	Lys	Tyr	His	Leu	Glu 155	Thr	Val	Ser	Asp	Leu 160
	Ala	Lys	His	Ser	Lys 165	Asp	Leu	Arg	Leu	Gly 170	Met	Asp	Ser	Ser	Trp 175	Met
35	Asn	Arg	Lys	Gly 180	Asp	Gly	Tyr	Glu	Gly 185	Phe	Lys	Lys	Glu	Tyr 190	Gly	Phe
	Asp	Phe	Gly 195	Thr	Val	Arg	Pro	Met 200	Gln	Ile	Gly	Leu	Val 205	Tyr	Asp	Ala
40	Leu	Asn 210	Ser	Glu	Lys	Leu	Asp 215	Val	Ala	Leu	Gly	Tyr 220	Ser	Thr	Asp	Gly
45	Arg 225	Ile	Ala	Ala	Tyr	Asp 230	Leu	Lys	Val	Leu	Lys 235	Asp	Asp	Lys	Gln	Phe 240
	Phe	Pro	Pro	Tyr	Ala 245	Ala	Ser	Ala	Val	Ala 250	Thr	Asn	Glu	Leu	Leu 255	Arg
50	Gln	His	Pro	Glu 260	Leu	Lys	Thr	Thr	Ile 265	Asn	Lys	Leu	Thr	Gly 270	Lys	Ile
	Ser	Thr	Ser 275	Glu	Met	Gln	Arg	Leu 280	Asn	Tyr	Glu	Ala	Asp 285	Gly	Lys	Gly
55	Lys	Glu 290	Pro	Ala	Val	Val	Ala 295	Glu	Glu	Phe	Leu	Lys 300	Lys	His	His	Tyr

Phe Asp Lys	Gln	Lys	Gly 310	Gly	His	Lys
TATEODAN TON	EOB I	CEO .	TIN NIC	). E1 (	٥.	

1	21	INFORMATION	FOR	SEO	ID	NO:5198:
٦,	41	THE OWNER TON	1 010			110.5150

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 284 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

15																
	(xi)	SEQU	JENCE	E DES	SCRIE	OITS	I: SE	EQ II	NO:	5198	3:					
22	Met 1	Lys	Lys	Leu	Thr 5	Thr	Leu	Leu	Leu	Ala 10	Ser	Thr	Leu	Leu	Ile 15	Ala
20	Ala	Cys	Gly	Asn 20	Asp	Asp	Ser	Lys	<b>Lys</b> 25	Asp	Asp	Ser	Lys	Thr 30	Ser	Lys
25	Lys	Asp	Asp 35	Gly	Val	Lys	Ala	Glu 40	Leu	Lys	Gln	Ala	Thr 45	Lys	Ala	Tyr
	Asp	Lys 50	Tyr	Thr	Asp	Glu	Gln 55	Leu	Asn	Glu	Phe	Leu 60	Lys	Gly	Thr	Glu
30	Lys 65	Phe	Val	Lys	Ala	Ile 70	Glu	Asn	Asn	Asp	Met 75	Ala	Gln	Ala	ГÀа	Ala 80
	Leu	Tyr	Pro	Lys	Val 85	Arg	Met	Tyr	Tyr	Glu 90	Arg	Ser	Glu	Pro	Val 95	Ala
35	Glu	Ala	Phe	Gly 100	Asp	Leu	Asp	Pro	Lys 105	Ile	Asp	Ala	Arg	Leu 110	Ala	Asp
	Met	Lys	Glu 115	Glu	Lys	Lys	Glu	Lys 120	Glu	Trp	Ser	Gly	Tyr 125	His	Lys	Ile
40	Glu	Lys 130	Ala	Leu	Туr	Glu	Asp 135	Lys	Lys	Ile	Asp	<b>Asp</b> 140	Val	Thr	Lys	Lys
	Asp 145		Gln	Gln	Leu	Leu 150	ГЛа	Asp	Ala	Lys	Glu 155	Leu	His	Ala	Lys	Ala 160
45	Asp	Thr	Leu	Asp	Ile 165	Thr	Pro	ГÀЗ	Leu	Met 170	Leu	Gln	Gly	Ser	Val 175	Asp
50	Leu	Leu	Asn	Glu 180	Val	Ala	Thr	Ser	Lys 185	Ile	Thr	Gly	Glu	Glu 190	Glu	Ile
	Tyr	Ser	His 195	Thr	Asp	Leu	Tyr	Asp 200	Phe	Lys	Ala	Asn	Val 205	Glu	Gly	Ala
55	Gln	Lys 210	Ile	Tyr	Asp	Leu	Phe 215	Lys	Pro	Ile	Leu	Glu 220	Lys	Lys	Asp	Lys

		Lys 225	Leu	Ser	Asp	Asp	Ile 230	Gln	Met	Asn	Phe	Asp 235	Lys	Val	Asn	Gln	Leu 240
5		Leu	Asp	Lys	Tyr	Lys 245	Asp	Asn	Asn	Gly	Gly 250	Tyr	Glu	Ser	Phe	Glu 255	Lys
		Val	Ser	Lys	Lys 260	Asp	Arg	Lys	Ala	Phe 265	Ala	Asp	Ala	Val	Asn 270	Ala	Leu
10		Gly	Glu	Pro 275	Leu	Ser	Lys	Met	Ala 280	Val	Ile	Thr	Glu				
	(2)	INFO	RMAT:	ION I	FOR S	SEQ I	D NO	0:519	99:								
15		(i)	(A) (B) (C)	JENCI LEN TYI STI	NGTH: PE: 39 RANDI	: 284 amino EDNES	ami aci SS: 8	ino a id singl	acids	3							
20		(ii)	MOLE	CUL	TY!	PE: p	prote	in									
25		(xi)	SEQU	JENCE	E DES	SCRIE	PTION	J: SE	EQ II	) <b>N</b> O:	5199	<b>)</b> :					
		Met 1	Lys	Lys	Leu	Thr 5	Thr	Leu	Leu	Leu	Ala 10	Ser	Thr	Leu	Leu	Ile 15	Ala
30		Ala	Cys	Gly	Asn 20	Asp	Asp	Ser	Lys	Lys 25	Asp	Asp	Ser	Lys	Thr 30	Ser	Lys
		Lys	Asp	Asp 35	Gly	Val	Lys	Ala	Glu 40	Leu	Lys	Gln	Ala	Thr 45	Lys	Ala	Tyr
35		Asp	Lys 50	Tyr	Thr	Asp	Glu	Gln 55	Leu	Asn	Glu	Phe	Leu 60	Lys	Gly	Thr	Glu
		Lys 65	Phe	Val	Lys	Ala	Ile 70	Glu	Asn	naA	Ąsp	Met 75	Ala	Gln	Ala	Lys	Ala 80
40		Leu	Tyr	Pro	Lys	Val 85	Arg	Met	Tyr	Tyr	Glu 90	Arg	Ser	Glu	Pro	Val 95	Ala
45		Glu	Ala	Phe	Gly 100	Asp	Leu	Asp	Pro	Lys 105	Ile	Asp	Ala	Arg	Leu 110	Ala	Asp
45		Met	Lys	Glu 115	Glu	Lys	Lys	Glu	Lys 120	Glu	Trp	Ser	Gly	Tyr 125	His	Lys	Ile
50		Glu	Lys 130	Ala	Leu	Tyr	Glu	Asp 135	Lys	Lys	Ile	Asp	Asp 140	Val	Thr	Lys	Lys
		<b>Asp</b> 145	Ala	Gln	Gln	Leu	Leu 150	Lys	Asp	Ala	Lys	Glu 155	Leu	His	Ala	Lys	Ala 160
55		Asp	Thr	Leu	Asp	Ile 165	Thr	Pro	Lys	Leu	Met 170	Leu	Gln	Gly	Ser	Val 175	Asp

		Leu	Leu	Asn	Glu 180	Val	Ala	Thr	Ser	Lys 185	Ile	Thr	Gly	Glu	Glu 190	Glu	Ile
5		Tyr	Ser	His 195	Thr	Asp	Leu	Tyr	<b>Asp</b> 200	Phe	Lys	Ala	Asn	<b>Val</b> 205	Glu	Gly	Ala
		Gln	Lys 210	Ile	Tyr	Asp	Leu	Phe 215	Lys	Pro	Ile	Leu	Glu 220	Lys	Lys	Asp	Lys
0		Lys 225	Leu	Ser	Asp	Asp	Ile 230	Gln	Met	Asn	Phe	Asp 235	Lys	Val	Asn	Gln	Leu 240
		Leu	Asp	Lys	Tyr	Lys 245	qaA	Asn	Asn	Gly	Gly 250	Tyr	Glu	Ser	Phe	Glu 255	Lys
15		Val	Ser	Lys	Lys 260	Asp	Arg	Lys	Ala	Phe 265	Ala	Asp	Ala	Val	Asn 270	Ala	Leu
		Gly	Glu	Pro 275	Leu	Ser	Lys	Met	<b>Ala</b> 280	Val	Ile	Thr	Glu				
?0	(2)	INFO	RMAT	ON I	FOR S	SEQ I	D NO	520	00:								
25		(i)	(A) (B) (C)	LEN TYI	E CHA NGTH: PE: & RANDI POLOC	208 mino EDNES	Bami baci SS: s	ino a id singl	cids	i							
		(ii)	MOL	ECUL	TYI	PE: p	prote	in									
30																	
		(xi)	SEQ	JENCE	E DES	SCRI	PTIO	1: SI	EQ II	NO:	:5200	<b>)</b> :					
35		Met 1	Lys	Phe	Lys	<b>Ala</b> 5	Ile	Val	Ala	Ile	Thr 10	Leu	Ser	Leu	Ser	<b>Leu</b> 15	Leu
		Thr	Ala	Cys	Gly 20	Ala	Asn	Gln	His	Lys 25	Glu	Asn	Ser	Ser	Lys 30	Ser	Asn
40		Asp	Thr	Asn 35	Lys	Lys	Thr	Gln	Gln 40	Thr	Asp	Asn	Thr	Thr 45	Gln	Ser	Asn
		Thr	Glu 50	Lys	Gln	Met	Thr	Pro 55	Gln	Glu	Ala	Glu	Asp 60	Ile	Val	Arg	Asn
<i>45</i>		Asp 65	Tyr	Lys	Ala	Arg	Gly 70	Val	Asn	Glu	Tyr	Gln 75	Thr	Leu	Asn	Tyr	Lys 80
50		Thr	Asn	Leu	Glu	Arg 85	Ser	Asn	Glu	His	Glu 90	Tyr	Tyr	Val	Glu	His 95	Leu
		Val	Arg	Asp	Ala 100	Val	Gly	Thr	Pro	Leu 105	Lys	Arg	Cys	Ala	Ile 110	Val	Asn
55		Arg	His	Asn 115	Gly	Thr	Ile	Ile	Asn 120	Ile	Phe	Asp	Asp	Met 125	Ser	Glu	Lys

		Asp	Lys 130	Glu	Glu	Phe	Glu	135	Phe	Lys	Lys	Arg	Ser 140	Pro	Lys	Tyr	Asn
5		Pro 145	Gly	Met	Asn	Asn	His 150	Asp	Glu	Thr	qaA	Gly 155	Glu	Ser	Glu	Asp	Ile 160
		Gln	His	His	Asp	Il <b>e</b> 165	Asp	Asn	Asn	Lys	Ala 170	Ile	Gln	Asn	Asp	Ile 175	Pro
10		Asp	Gln	Lys	Val 180	Asp	Asp	Lys	Asn	Asp 185		Asn	Ala	Val	Asn 190	Lys	Glu
15		Glu	Lys	His 195	Asp	Asn	Gly	Ala	Asn 200		Ser	Glu	Glu	Thr 205	Lys	Val	Lys
15	(2)	INFO	RMAT	ION :	FOR	SEQ	ID N	0:52	01:								
20		(i)	(A (B (C	UENC: ) LEI ) TY: ) STI ) TO:	NGTH PE: RAND	: 18 amin EDNE:	4 am o ac SS:	ino a id sing:	acid	s							
25		(ii)	MOL	ECULI	E TY:	PE: ]	prote	ein									
		(xi)	SEQ	UENCI	E DES	SCRI	PTIO	N: S1	EQ II	ои с	:520:	1:					
30		Met 1	Leu	Lys	Gly	Cys 5	Gly	Gly	Cys	Leu	Ile 10	Ser	Phe	Ile	Leu	Leu 15	Ile
		Ile	Leu	Leu	Ser 20	Ala	Cys	Ser	Met	Met 25	Phe	Ser	Asn	Asn	Asp 30	Asn	Ser
35		Thr	Asn	Asn 35	Gln	Ser	Ser	Lys	Thr 40	Gln	Leu	Thr	Gln	Lys 45	Asp	Glu	Asn
40		Lys	Asn 50	Glu	Asp	Lys	Pro	Glu 55	Glu	Lys	Ser	Glu	Thr 60	Ala	Thr	Asp	Glu
		Asp 65	Leu	Gln	Ser	Thr	Glu 70	Glu	Val	Pro	Ala	Asn 75	Glu	Asn	Thr	Glu	Asn 80
45		Asn	Gln	His	Glu	Ile 85	Asp	Glu	Ile	Thr	Thr 90	Lys	Asp	Gln	Ser	Asp 95	Asp
		Asp	Ile	Asn	Thr 100	Pro	Asn	Val	Ala	Glu 105	Asp	Lys	Ser	Gln	Asp 110	Asp	Leu
50		Lys	Asp	<b>Asp</b> 115	Leu	Lys	Glu	Lys	Gln 120	Gln	Ser	Ser	Asn	His 125	His	Gln	Ser
		Thr	Gln 130	Pro	Lys	Thr	Ser	Pro 135	Ser	Thr	Glu	Thr	Asn 140	Thr	Gln	Gln	Ser
55		Phe	Ala	Asn	Cys	Lys	Gln	Leu	Arg	Gln	Val	Tyr	Pro	Asn	Gly	Val	Thr

	Ala	Asp	His	Pro	Ala 165	Tyr	Arg	Pro	His	Leu 170	Asp	Arg	Asp	Lys	Asp 175	ГÀЗ
5	Arg	Ala	Cys	Glu 180	Pro	Asp	Lys	Tyr								
(	2) INFOR	MATI	ON F	OR S	EQ 1	D NO	:520	2:								
10	(i)	(B)	LEN TYP STR	IGTH: PE: a LANDE	208 mino EDNES	TERIS  ami aci SS: s linea	no a .d singl	cids	1							
15	(ii)	MOLE	ECULE	TYF	PE: p	rote	in									
20	(xi)	SEQU	JENCE	DES	SCRI	PTION	1: SI	EQ II	NO:	5202	2:					
	Met 1	Lys	Lys	Arg	Leu 5	Leu	Leu	Ser	Thr	Phe 10	Leu	Ala	Ser	Thr	Leu 15	Ile
25	Leu	Thr	Gly	Cys 20	Ala	Ser	Asp	Gln	Ser 25	Asp	Asn	Glu	Asp	His 30	His	Thr
	Ser	Thr	Gly 35	Ile	His	Ala	Pro	Lys 40	Ser	Ala	Lys	Lys	Leu 45	Glu	Thr	Lys
30	Asp	Ile 50	Phe	Xaa	Ser	Asp	Lys 55	Lys	Asn	Ser	Asp	Ile 60	Ser	Asp	Ala	Glu
	Met 65	Lys	Gln	Ala	Ile	Glu 70	ГÀЗ	Tyr	Leu	Ser	<b>V</b> al 75	Asn	Ser	Asp	Ile	Leu 80
35	Asp	Asn	Lys	Tyr	Ile 85	Met	Gln	His	Lys	Leu 90	Asp	Lys	Gln	Ile	Asp 95	Ser
	Gln	Thr	Lys	Val 100	Thr	Glu	Lys	Gln	Ala 105	Glu	Thr	Leu	Ser	His 110	Leu	Ser
40	Asn	Leu	Ala 115	Val	Lys	Asn	Asp	Leu 120	His	Phe	Lys	Lys	Phe 125	Val	Thr	Glu
45	Asn	Asn 130	Ile	Pro	Lys	Glu	Tyr 135	Lys	Lys	Pro	Val	Glu 140	Leu	Met	Met	Asn
	Tyr 145	Phe	Lys	Ala	Leu	<b>A</b> sn 150	Ser	Thr	Ile	Ala	Asn 155	Val	Asp	Glu	Asp	Ile 160
50	Glu	Lys	Leu	Ser	Tyr 165		Pro	Gln	Asn	Lys 170	Ile	Asn	Val	Val	Asp 175	Val
	Pro	Thr	Lys	Tyr 180		Gly	Asp	Val	Asn 185	Lys	Lys	Gln	Gln	Asp 190	Lys	Ile
55	Lys	Asp	Phe	Leu	Lys	Ser	Lys	Gly	Ile	Lys	Ser	Asp	Val	Ile	Asp	Lys

(2) INFORMATION FOR SEQ ID NO:5203:

5	(i)	(A (B (C	) LE: ) TY ) ST:	E CHANGTH PE: 6 RANDI POLO	: 28 amine EDNE:	3 am cac ss:	ino a id sing:	acid	S							
10	(ii)	MOL	ECUL	E TY	PE: ]	prote	ein									
15	(xi)	SEQ	UENC	E DES	SCRI	PTIO	N: S1	EQ II	ON O	:520	3 :					
	Met 1	Lys	Ser	Lys	Ile 5	Tyr	Ile	Leu	Leu	Leu 10	Xaa	Leu	Ile	Phe	Leu 15	Ser
20	Ala	Cys	Ala	Asn 20	Thr	Arg	His	Ser	Glu 25	Ser	Asp	Lys	Asn	Val 30	Leu	Thi
	Val	Tyr	Ser 35	Pro	Tyr	Gln	Ser	Asn 40	Leu	Ile	Arg	Pro	Ile 45	Leu	Asn	Glu
25	Xaa	Glu 50	Lys	Gln	Glu	His	Val 55	Lys	Ile	Glu	Ile	Lys 60	His	Gly	Ser	Thr
	Gln 65	Val	Leu	Leu	Ser	Asn 70	Leu	His	Asn	Glu	Asp 75	Phe	Ser	Glu	Arg	Gly 80
30	Asp	Val	Phe	Met	Gly 85	Gly	Val	Leu	Ser	Glu 90	Thr	Ile	Asp	His	Pro 95	Glu
	Asp	Phe	Val	Pro 100	Tyr	Gln	Asp	Thr	Ser 105	Val	Thr	Gln	Gln	Leu 110	Glu	Asp
35	Tyr	Arg	Ser 115	Asn	Asn	Lys	Tyr	Val 120	Thr	Ser	Phe	Leu	Leu 125	Met	Pro	Thr
40	Val	Ile 130	Val	Val	Asn	Ser	Asp 135	Leu	Gln	Gly	Asp	Ile 140	Lys	Ile	Arg	Gly
	Tyr 145	Gln	Asp	Leu	Leu	Gln 150	Pro	Ile	Leu	Lys	Gly 155	Lys	Ile	Ala	Tyr	Ser 160
45	Asn	Pro	Asn	Thr	Thr 165	Thr	Thr	Gly	Tyr	Gln 170	His	Met	Arg	Ala	Ile 175	Туг
	Ser	Met	His	His 180	Arg	Val	Ser	Asp	Val 185	His	Gln	Phe	Gln	<b>As</b> n 190	His	Ala
50	Met	Gln	Leu 195	Ser	Lys	Thr	Ser	Lys 200	Val	Ile	Glu	Asp	Val 205	Ala	Lys	Gly
	Lys	Tyr	Tyr	Ala	Gly	Leu	Ser	Tyr	Glu	Gln	Asp	Ala	Arg	Thr	Trp	Lys

		225					230					235					240
5		Leu	Asn	Val	Asp	Gly 245	Ile	Ala	Leu	Val	Lys 250	Asn	Ala	His	Pro	His 255	Pro
,		Lys	Arg	Lys	Lys 260	Leu	Val	Gln	Tyr	Leu 265	Thr	Ser	Arg	Ser	<b>Val</b> 270	Gln	Gln
0		Arg	Leu	Val 275	Ala	Glu	Phe	Asp	Ala 280	Lys	Ser	Ile					
	(2)	INFO	RMAT	ION I	FOR S	SEQ 1	D NO	520	14:								
15		(i)	(A) (B) (C)	LEN TYI	NGTH PE: 8 RANDI	ARACT : 309 amino EDNES GY: ]	ami aci SS: £	ino a id singl	cids	3							
20		(ii)	MOLI	ECULI	E TYI	PE: p	rote	ein									
		(xi)	SEQ	JENCI	E DES	SCRIE	PTIO	N: SI	EQ II	NO:	: 5204	<b>1</b> :					
25		Met 1	Lys	Lys	Phe	Ile 5	Gly	Ser	Val	Leu	Ala 10	Thr	Thr	Leu	Ile	Leu 15	Gly
		Gly	Сув	Ser	Thr 20	Met	Glu	Asn	Glu	Ser 25	Lys	Lys	Asp	Thr	Lys	Thr	Glu
30		Thr	Lys	Ser 35	Val	Pro	Glu	Glu	Met 40	Glu	Ala	Ser	Lys	Tyr 45	Val	Gly	Gln
35		Gly	Phe 50	Gln	Pro	Pro	Ala	Glu 55	Lys	Asn	Ala	Ile	Glu 60	Phe	Ala	Lys	Lys
		His 65	Arg	Lys	Glu	Phe	Glu 70	Lys	Val	Gly	Glu	Gln 75	Phe	Phe	Lys	Asp	Asn 80
40		Phe	Gly	Leu	Lys	Val 85	Lys	Ala	Thr	Asn	<b>Val</b> 90	Val	Gly	Lys	Asp	<b>As</b> p 95	Gly
		Val	Glu	Val	Tyr 100	Val	His	Сув	Glu	<b>As</b> p 105	His	Gly	Ile	Val	Phe 110	Asn	Ala
45		Ser	Leu	Pro 115	Leu	Tyr	Lys	Asp	Ala 120	Ile	His	Gln	Lys	Gly 125	Ser	Met	Arg
		Ser	Asn 130	Asp	Asn	Gly	Asp	Asp 135	Met	Ser	Met	Met	Val 140	Gly	Thr	Val	Leu
50		Ser 145	Gly	Phe	Glu	Tyr	Arg 150	Ala	Gln	Lys	Glu	Lys 155	Tyr	Asp	Asn	Leu	<b>Tyr</b> 160
		Lys	Phe	Phe	Lys	Glu	Asn	Glu	Lys	Lys	Tyr		Tyr	Thr	Gly	Phe	Thr

					180					185					190		
5		Phe	Tyr	Ile 195	Thr	Tyr	Ser	Ser	Arg 200	Ser	Leu	Lys	Glu	Tyr 205	Arg	Lys	Туг
Ū		Tyr	Glu 210	Pro	Leu	Ile	Arg	Lys 215	Asn	Asp	Lys	Glu	Phe 220	Lys	Glu	Gly	Met
10		Glu 225	Arg	Ala	Arg	Lys	Glu 230	Val	Asn	Tyr	Ala	Ala 235	Asn	Thr	Asp	Ala	Val 240
		Ala	Thr	Leu	Phe	Ser 245	Thr	Lys	Lys	Asn	Phe 250	Thr	Lys	Asp	Asn	Thr 255	Val
15		Asp	Asp	Val	Ile 260	Glu	Leu	Ser	Asp	<b>Lys</b> 265	Leu	Tyr	Asn	Leu	Lys 270	Asn	Lys
		Pro	Asp	Lys 275	Ser	Thr	Ile	Thr	Ile 280	Gln	Ile	Gly	Lys	Pro 285	Thr	Ile	Asn
20		Thr	Lys 290	Lys	Ala	Phe	Tyr	Asp 295	Asp	Asn	Arg	Pro	Ile 300	Glu	Tyr	Gly	Val
		His 305	Ser	Lys	Asp	Glu											
25	(2)	INFO	RMAT	ION I	FOR S	SEQ I	ID NO	):520	)5:								
30		(i)	(A) (B) (C)	LEI TYI STI	NGTH: PE: & RANDI	: 193	3 am: 5 ac: 55: s	singl	acids	3							
		(ii)	MOLE	CUL	E TYP	PE: p	rote	ein									
35																	
		(xi)	SEQU	JENCI	E DES	SCRIE	PTION	I: SE	Q II	NO:	5205	<b>5</b> :					
40		Met 1	Lys	Lys	Leu	<b>Val</b> 5	Ser	Ile	Val	Gly	Ala 10	Thr	Leu	Leu	Leu	Ala 15	Gly
		Cys	Gly	Ser	Gln 20	Asn	Leu	Ala	Pro	Leu 25	Glu	Glu	Lys	Thr	Thr 30	Asp	Leu
45		Arg	Glu	Asp 35	Asn	His	Gln	Leu	Lys 40	Leu	Asp	Ile	Gln	Glu 45	Leu	Asn	Gln
		Gln	Ile 50	Ser	Asp	Ser	Lys	Ser 55	Lys	Ile	Lys	Gly	Leu 60	Glu	Lys	Asp	Lys
50		Glu 65	Asn	Ser	Lys	Lys	Thr 70	Ala	Ser	Asn	Asn	Thr 75	Lys	Ile	Lys	Leu	Met 80
		Asn	Val	Thr	Ser	Thr 85	Tyr	Tyr	Asp	Lys	Val 90	Ala	Lys	Ala	Leu		Ser
55											J 0					95	

					100					105					110		
		Val	Gln	Ser 115	ГХа	Leu	Asn	Gln	Ile 120	Ser	Asn	Asp	Ile	Gln 125	Ser	Ala	His
5		Thr	Ser 130	Tyr	Lys	Asp	Ala	Ile 135	Asp	Gly	Leu	Ser	Leu 140	Ser	Asp	Asp	Asp
10		<b>Lys</b> 145	Lys	Thr	Ser	Lys	<b>As</b> n 150	Ile	Asp	Lys	Leu	Asn 155	Ser	Asp	Leu	Asn	His 160
		Ala	Phe	Asp	Asp	Ile 165	Lys	Asn	Gly	Tyr	Gln 170	Asn	Lys	Asp	Lys	Lys 175	Glr
15		Leu	Thr	Lys	Gly 180	Gln	Gln	Ala	Leu	Ser 185	Lys	Leu	Asn	Leu	<b>As</b> n 190	Ala	Lys
		Ser															
20	(2)	INFO	RMAT:	I NOI	FOR S	EQ 1	ID N	0:52	06:								
25		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 8 RANDI	ARACT 259 Amino EDNES	e am: c ac: SS: 8	ino a id sing]	acida	5							
		(ii)															
30																	
		(xi)	SEQ	JENC	E DES	SCRII	PTIO	N: SI	EQ II	ON C	: 520	5:					
35		Met 1	Lys	Arg	Leu	Leu 5	Phe	Val	Met	Ile	Ala 10	Phe	Val	Phe	Ile	Leu 15	Ala
		Ala	Суѕ	Gly	Asn 20	Asn	Ser	Ser	Lys	<b>Asp</b> 25	Lys	Glu	Ala	Ser	Lys 30	_	Se
40		Lys	Thr	Ile 35	Asn	Val	Gly	Thr	Glu 40	Gly	Thr	Tyr	Ala	Pro 45	Phe	Ser	Phe
		His	Asp 50	Lys	Asp	Gly	Lys	<b>Le</b> u 55	Thr	Gly	Tyr	Asp	Ile 60	Asp	Val	Ile	Lys
45		Ala 65	Val	Ala	Lys	Glu	Glu 70	Gly	Leu	Lys	Leu	Lys 75	Phe	Asn	Glu	Thr	Ser 80
		Trp	Asp	Ser	Met	Phe 85	Ala	Gly	Leu	Asp	Ala 90	Gly	Arg	Phe	Asp	Val 95	Ile
50		Ala	Asn	Gln	Val 100	Gly	Ile	Asn	Pro	Asp 105	Arg	Glu	Lys	Lys	Tyr 110	Lys	Phe
		Ser	Lys	Pro	Tyr	Thr	Phe	Ser	Ser 120	Ala	Val	Leu	Val	Ile 125	Arg	Glu	Ası

			130					135					140				
5		Gln 145	Thr	Phe	Thr	Ser	Asn 150	Tyr	Gly	Lys	Leu	Ala 155	Lys	Asp	Lys	Gly	Ala 160
		Asp	Ile	Thr	Lys	Val 165	Asp	Gly	Phe	Asn	Gln 170	Ser	Met	Asp	Leu	Leu 175	Le
10		Ser	Lys	Arg	<b>Val</b> 180	Asp	Gly	Thr	Phe	<b>As</b> n 185	Asp	Ser	Leu	Ser	Tyr 190	Leu	Asp
		Tyr	Lys	Lys 195	Gln	Lys	Pro	Asn	Ala 200	Lys	Ile	Lys	Ala	Ile 205	Lys	Gly	Asr
15		Ala	Glu 210	Gln	Ser	Arg	Ser	Ala 215	Phe	Ala	Phe	Ser	Lys 220	Lys	Ala	Asp	Asp
		Glu 225	Thr	Val	Gln	Lys	Phe 230	Asn	Asp	Gly	Leu	Lys 235	Lys	Ile	Glu	Glu	Asr 240
20		Gly	Glu	Leu	Ala	Lys 245	Ile	Gly	Lys	Lys	Trp 250	Phe	Gly	Gln	Asp	Val 255	Ser
		Lys	Ser	Lys													
25	(2)	INFOR	TAMS	ON I	FOR S	SEQ :	ID NO	0:520	7:								
30		<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 203 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>															
		(ii)	MOLE	CUL	E TYI	PE: p	prote	ein									
35																	
		(xi)	SEQU	JENCE	E DES	CRIE	PTION	l: SE	EQ II	NO:	5207	7:					
40		Met 1	Gly	Val	His	Ser 5	Met	Lys	Leu	Lys	Arg 10	Leu	Phe	Ala	Val	Val 15	Ile
		Ala	Met	Leu	Leu 20	Val	Leu	Ala	Gly	Cy <b>s</b> 25	Ser	Asn	Ser	Asn	Asp 30	Asn	Asn
45		Glu	Ser	Lys 35	Lys	Asp	qaA	Ala	Asp 40	Asn	Gly	Lys	Lys	Gln 45	Glu	Ile	Gln
		Val	Ala 50	Ala	Ala	Ala	Ser	Leu 55	Thr	Asp	Val	Thr	Lys 60	Lys	Leu	Ala	Ser
50		Glu 65	Phe	Lys	Lys	Glu	His 70	Lys	Asn	Ala	Asp	Ile 75	Lys	Phe	Asn	Tyr	Gly 80
		Gly	Ser	Gly	Ala	Leu 85	Arg	Lys	Gln	Ile	Glu 90	Ser	Gly	Ala	Pro	<b>Val</b> 95	Asp

					100					105					110		
5		Asn	Lys	Ala 115	His	Asp	Thr	Tyr	Lys 120	Tyr	Ala	Lys	Asn	Ser 125	Leu	Val	Leu
J		Ile	Gly 130	Asp	Lys	Asp	Ser	Asn 135	Tyr	Thr	Ser	Val	Lys 140	Asp	Leu	Lys	Asp
10		Asn 145	Asp	Lys	Leu	Ala	Leu 150	Gly	Glu	Val	Lys	Thr 155	Val	Pro	Ala	Gly	Lys 160
		Tyr	Ala	Lys	Gln	Tyr 165	Leu	Asp	Asn	Asn	<b>As</b> n 170	Leu	Phe	Lys	Glu	Val 175	Glu
15		Ser	Xaa	Ile	Val 180	Tyr	Ala	Lys	Asp	Val 185	Lys	Gln	Val	Leu	Asn 190	Tyr	Val
		Xaa	Lys	Gly 195	Asn	Ala	Lys	Gln	Gly 200	Phe	Val	Tyr					
20	(2)	INFOR	TAMS	ION I	FOR S	SEQ I	D NO	0:520	8:								
25		(i)	(A) (B) (C)	LEI TYI STI	E CHA NGTH: PE: 8 RANDI POLO	: 327 amino EDNES	7 ami 5 aci 55: 5	ino a id sing:	acids	3							
		(ii)	MOLI	ECULI	E TY	PE: p	prote	ein									
30																	
		(xi)	SEQ	JENCI	E DES	SCRII	PTIO	N: SI	EQ II	ON O	: 5208	3 :					
35		Met 1	Lys	Lys	Trp	Gln 5	Phe	Val	Gly	Thr	Thr 10	Ala	Leu	Gly	Ala	Thr 15	Leu
		Leu	Leu	Gly	Ala 20	Cys	Gly	Gly	Gly	Asn 25	Gly	Gly	Ser	Gly	Asn 30	Ser	Asp
40		Leu	Lys	Gly 35	Glu	Ala	Lys	Gly	<b>Asp</b> 40	Gly	Ser	Ser	Thr	Val 45	Ala	Pro	Ile
		Val	Glu 50	Lys	Leu	Asn	Glu	<b>Lys</b> 55	Trp	Ala	Gln	Asp	His 60	Ser	Asp	Ala	Lys
45		Ile 65	Ser	Ala	Gly	Gln	Ala 70	Gly	Thr	Gly	Ala	Gly 75	Phe	Gln	Lys	Phe	Ile 80
		Ala	Gly	Asp	Ile	Asp 85	Phe	Ala	Asp	Ala	Ser 90	Arg	Pro	Ile	Lys	Asp 95	Glu
50		Glu	Lys	Gln	Lys 100	Leu	Gln	Asp	Lys	Asn 105	Ile	Lys	Tyr	Lys	Glu 110	Phe	Lys
		Ile	Ala	Gln 115	Asp	Gly	Val	Thr	Val 120	Ala	Val	Asn	Lys	Glu 125	Asn	Asp	Phe

5		Ala 145	Lys	Thr	Trp	Lys	<b>Asp</b> 150	Val	Asn	Ser	Lys	Trp 155	Pro	Asp	Lys	Lys	Ile 160
		Asn	Ala	Val	Ser	Pro 165	Asn	Ser	Ser	His	Gly 170	Thr	Tyr	Asp	Phe	Phe 175	Glu
10		Asn	Glu	Val	Met 180	Asn	Lys	Glu	Asp	Ile 185	Lys	Ala	Glu	Lys	Asn 190	Ala	Asp
		Thr	Asn	Ala 195	Ile	Val	Ser	Ser	Val 200	Thr	Lys	Asn	Lys	Glu 205	Gly	Ile	Gly
15		Tyr	Phe 210	Gly	Tyr	Asn	Phe	Tyr 215	Val	Gln	Asn	Lys	<b>Asp</b> 220	Lys	Leu	Lys	Glu
		Val 225	Lys	Ile	Lys	Asp	Glu 230	Asn	Gly	Lys	Ala	Thr 235	Glu	Pro	Thr	Lys	Lys 240
20		Thr	Ile	Gln	Asp	Asn 245	Ser	Tyr	Ala	Leu	Ser 250	Arg	Pro	Leu	Phe	Ile 255	Tyr
		Val	Asn	Glu	<b>Lys</b> 260	Ala	Leu	Lys	Asp	<b>Asn</b> 265	Lys	Val	Met	Ser	Glu 270	Phe	Ile
25		Lys	Phe	<b>Val</b> 275	Leu	Glu	Asp	Lys	Gly 280	Lys	Ala	Ala	Glu	Glu 285	Ala	Gly	Tyr
20		Val	Ala 290	Ala	Pro	Glu	Lys	Thr 295	Tyr	Lys	Ser	Gln	Leu 300	Asp	Asp	Leu	Lys
30		Ala 305	Phe	Ile	Asp	Lys	Asn 310	Gln	Lys	Ser	Asp	Asp 315	Lys	Lys	Ser	Asp	<b>As</b> p 320
35		Lys	Lys	Ser	Glu	Asp 325	Lys	Lys									
	(2)	INFOR	TAMS:	ON E	FOR S	SEQ I	D NO	520	9:								
40		(i)	(A) (B) (C)	LEN TYPE	E CHA NGTH: PE: a RANDE	: 324 amino EDNES	ami aci SS: s	no a d singl	cids	3							
		(ii)	MOLE	CULE	TYP	E: r	rote	in									
45																	
		(xi)	SEQU	JENCE	E DES	CRIE	MOIT	I: SE	EQ II	NO:	5209	):					
50		Met 1	Lys	Arg	Leu	Ser 5	Ile	Ile	Val	Ile	Ile 10	Gly	Ile	Phe	Ile	Ile 15	Thr
		Gly	Cys	Asp	Trp 20	Gln	Arg	Thr	Ser	Lys 25	Glu	Arg	Ser	Lys	Asn 30	Ala	Gln
55																	

40 45 35 Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys 5 Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu 10 Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 15 Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His Arg Tyr Ser Thr His Tyr Leu Leu Glu Glu Leu Arg Lys Gln Leu 20 Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 25 Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 30 Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 35 Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 40 Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 280 Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 45 295 Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 310 315

(2) INFORMATION FOR SEQ ID NO:5210:

Ala Ser Arg Ser

50

55

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5		(ii)	MOL	ECUL	Е ТҮ	PE:	prot	ein									
10		(xi)	SEQ	UENC:	E DE:	SCRI	PTIO	N: S	EQ II	on o	:521	0 :					
		Met 1	Lys	Lys	Thr	Leu 5	Gly	Суз	Leu	Leu	Leu 10	Ile	Met	Leu	Leu	Val 15	Val
15		Ala	Gly	Cys	Ser 20	Phe	Gly	Gly	Asn	His 25	Lys	Leu	Ser	Ser	Lys 30	Lys	Ser
		Glu	Glu	Ser 35	Lys	Gln	Glu	Thr	Val 40	Lys	Lys	Glu	Ser	Glu 45	Glu	Glu	Lys
20		Asp	Pro 50	Asp	Leu	Glu	Lys	Tyr 55	Glu	Glu	Ile	Glu	Lys 60	Lys	Met	Lys	Gly
		Ile 65	Lys	Asp	Ala	Pro	Ser 70	Leu	Asp	Lys	Leu	Asp 75	Pro	Leu	Met	Thr	Glu 80
25		Lys	Ser	Phe	Thr	Asn 85	Ser	Lys	Gly	Ile	Gln 90	Gly	Trp	Lys	Asp	Tyr 95	Lys
00		Glu	Leu	Met	Gly 100	Lys	Val	Glu	Leu	Ala 105	Asp	Tyr	Arg	Phe	Thr 110	Lys	Asp
30		Ser	Lys	Gly 115	Ser	Ser	Ile	Lys	<b>Asp</b> 120	Val	Asp	Ala	Phe	Phe 125	Lys	Gly	Lys
35		Lys	Gly 130	Ile	ГÀЗ	Arg	Lys	Val 135	Ile	Glu	Thr	His	Asp 140	Asp	Val	Lys	Gln
		Val 145	Asp	Tyr	Trp												
40	(2)	INFOR															
		(1)	(B)	LEN TY	NGTH:	: 33 amino	renis amir aci SS: s	no ac	cids								
<b>4</b> 5		(;;)	(D)	TOE	POLOC	3Y: ]	linea	ır	_								
		(ii)	МОБЕ	CODE	. 111	e: I	roce	in									
50		(xi)	SEQU	JENCE	E DES	SCRIE	PTION	I: SE	Q II	NO:	521	L:					
		Trp 1	Pro	Сув	Ala	Thr 5	Xaa	Gln	Glx	Glu	Trp 10	Trp	Ser	Arg	His	Xaa 15	Trp
55																	

		His															
5	(2)	INFOR	RMATI	ON F	OR S	SEO I	ID NO	:521	L <b>2</b> :								
10	(2)		SEQU (A) (B) (C)	JENCE LEN TYP STR	CHA IGTH: PE: a	RACT 490 mino	reris	STICS .no a .d singl	3: acids	<b>;</b>							
15		(ii)	MOLE	ECULE	TYP	E: p	prote	ein									
		(xi)	SEQU	JENCE	E DES	CRIE	PTION	I: SI	SQ II	NO:	5212	: :					
20		Met 1	Ser	Ile	Ile	Met 5	Glu	Val	Ala	Thr	Met 10	Gln	Ala	Lys	Leu	Thr 15	Lys
		Asn	Glu	Phe	Ile 20	Glu	Trp	Leu	Lys	Thr 25	Ser	Glu	Gly	Lys	Gln 30	Phe	Asn
25		Val	Asp	Leu 35	Trp	Tyr	Gly	Phe	Gln 40	Cys	Phe	Asp	Tyr	Ala 45	Asn	Ala	Gly
		Trp	Lys 50	Val	Leu	Phe	Gly	Leu 55	Leu	Leu	Lys	Gly	<b>Le</b> u 60	Gly	Ala	Lys	Asp
30		Ile 65	Pro	Phe	Ala	Asn	Asn 70	Phe	Asp	Gly	Leu	Ala 75	Thr	Val	Tyr	Gln	Asn 80
35		Thr	Pro	Asp	Phe	Leu 85	Ala	Gln	Pro	Gly	Asp 90	Met	Val	Val	Phe	Gly 95	Ser
		Asn	Tyr	Gly	Ala 100	Gly	Tyr	Gly	His	Val 105	Ala	Trp	Val	Ile	Glu 110	Ala	Thr
40		Leu	Asp	Tyr 115	Ile	Ile	Val	Tyr	Glu 120	Gln	Asn	Trp	Leu	Gly 125	Gly	Gly	Trp
		Thr	Asp 130	Gly	Ile	Glu	Gln	Pro 135	Gly	Trp	Gly	Trp	Glu 140	Lys	Val	Thr	Arg
45		Arg 145	Gln	His	Ala	Tyr	<b>Asp</b> 150	Phe	Pro	Met	Trp	Phe 155	Ile	Arg	Pro	Asn	Phe 160
		Lys	Ser	Glu	Thr	Ala		Arg	Ser	Val	Gln 170		Pro	Thr	Gln	Ala 175	

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile 

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn 195 200 205

5		Ala 225	Glu	Ala	Tyr	Arg	<b>Asn</b> 230	Gly	Leu	Val	Asn	Ala 235	Pro	Leu	Ser	Arg	Leu 240
		Glu	Ala	Gly	Ile	Ala 245	His	Ser	Tyr	Val	Ser 250	Gly	Asn	Thr	Val	Trp 255	Gln
10		Ala	Leu	Asp	Glu 260	Ser	Gln	Val	Gly	Trp 265	His	Thr	Ala	Asn	Gln 270	Ile	Gly
		Asn	Lys	Tyr 275	Tyr	Tyr	Gly	Ile	Glu 280	Val	Cys	Gln	Ser	Met 285	Gly	Ala	Asp
15		Asn	Ala 290	Thr	Phe	Leu	Lys	Asn 295	Glu	Gln	Ala	Thr	Phe 300	Gln	Glu	Cys	Ala
		<b>Arg</b> 305	Leu	Leu	Lys	ГÀЗ	Trp 310	Gly	Leu	Pro	Ala	<b>As</b> n 315	Arg	Asn	Thr	Ile	Arg 320
20		Leu	His	Asn	Glu	Phe 325	Thr	Ser	Thr	Ser	Cys 330	Pro	His	Arg	Ser	Ser 335	Val
		Leu	His	Thr	Gly 340	Phe	Asp	Pro	Val	Thr 345	Arg	Gly	Leu	Leu	Pro 350	Glu	Asp
25		Lys	Arg	Leu 355	Gln	Leu	Lys	Asp	Tyr 360	Phe	Ile	Lys	Gln	Ile 365	Arg	Ala	Tyr
		Met	<b>Asp</b> 370	Gly	Lys	Ile	Pro	Val 375	Ala	Thr	Val	Ser	Asn 380	Glu	Ser	Ser	Ala
30		Ser 385	Ser	Asn	Thr	Val	Lys 390	Pro	Val	Ala	Ser	Ala 395	Trp	Lys	Arg	Asn	Lys 400
35		Tyr	Gly	Thr	Tyr	Tyr 405	Met	Glu	Glu	Ser	Ala 410	Arg	Phe	Thr	Asn	Gly 415	Asn
		Gln	Pro	Ile	Thr 420	Val	Arg	ГÀЗ	Val	Gly 425	Pro	Phe	Leu	Ser	Cys 430	Pro	Val
40		Gly	Tyr	Gln 435	Phe	Gln	Pro	Gly	Gly 440	Tyr	Cys	Asp	Tyr	Thr 445	Glu	Val	Met
		Leu	Gln 450	Asp	Gly	His	Val	Trp 455	Val	Gly	Tyr	Thr	Trp 460	Glu	Gly	Gln	Arg
45		Tyr 465	Tyr	Leu	Pro	Ile	Arg 470	Thr	Trp	Asn	Gly	Ser 475	Ala	Pro	Pro	Asn	Gln 480
		Ile	Leu	Gly	Asp	Leu 485	Trp	Gly	Glu	Ile	Ser 490						
50	(2)	INFO	TAMS	ON F	FOR S	SEQ 1	D NO	521	L3:								
		(i)		JENCE LEN	IGTH :	299	ami	ino a		5							
55				STF					le								

# (ii) MOLECULE TYPE: protein

5																
	(xi)	SEQ	UENCI	E DES	SCRI	PTIO	N: S	EQ II	ON C	: 521	3 :					
10	Gly 1	Asp	Lys	Met	Asn 5	Lys	Ile	Ser	Lys	Tyr 10	Ile	Ala	Ile	Ala	Ser 15	Leu
	Ser	Val	Ala	Val 20	Thr	Val	Ser	Ala	Pro 25	Gln	Thr	Thr	Asn	Ser 30	Thr	Ala
15	Phe	Ala	Lys 35	Ser	Ser	Ala	Glu	Val 40	Gln	Gln	Thr	Gln	Gln 45	Ala	Ser	Ile
	Pro	Ala 50	Ser	Gln	Lys	Ala	Asn 55	Leu	Gly	Asn	Gln	Asn 60	Ile	Met	Ala	Val
20	Ala 65	Trp	Tyr	Gln	Asn	Ser 70	Ala	Glu	Ala	Lys	Ala 75	Leu	Tyr	Leu	Gln	Gly 80
25	Tyr	Asn	Ser	Ala	Lys 85	Thr	Gln	Leu	Asp	90 Tàa	Glu	Ile	Lys	Lys	Asn 95	Lys
	Gly	Lys	His	Lys 100	Leu	Ala	Ile	Ala	Leu 105	Asp	Leu	Asp	Glu	Thr 110	Val	Leu
30	Asp	Asn	<b>Ser</b> 115	Pro	Tyr	Gln	Gly	Tyr 120	Ala	Ser	Ile	His	Asn 125	Lys	Pro	Phe
	Pro	Glu 130	Gly	Trp	His	Glu	Trp 135	Val	Gln	Ala	Ala	Lys 140	Ala	Lys	Pro	Val
35	Tyr 145	Gly	Ala	Lys	Glu	Phe 150	Leu	Lys	Tyr	Ala	<b>Asp</b> 155	Lys	Lys	Gly	Val	<b>As</b> p 160
40		_			165	_			_	170	_	_		Lys	175	
40	Gln	Lys	Asn	Leu 180	Lys	Gln	Gln	Gly	Ile 185	Pro	Gln	Ala	Lys	Lys 190	Ser	His
45	Ile	Leu	Leu 195	Lys	Gly	Lys	Asp	<b>Asp</b> 200	Lys	Ser	Lys	Glu	Ser 205	Arg	Arg	Gln
	Met	Val 210	Gln	Lys	Asp	His	Lys 215	Leu	Val	Met	Leu	Phe 220	Gly	Asp	Asn	Leu
50	Leu 225	Asp	Phe	Thr	Asp	Pro 230	Lys	Glu	Ala	Thr	Ala 235	Glu	Ser	Arg	Glu	Ala 240
	Leu	Ile	Glu	Lys	His 245	Lys	Asp	Asp	Phe	Gly 250	Lys	Lys	Tyr	Ile	Ile 255	Phe
55	Pro	Asn	Pro	Met 260	Tyr	Gly	Ser	Trp	Glu 265	Ala	Thr	Ile	Tyr	<b>As</b> n 270	Asn	Asn

				275					280					285			
5		Lys	Gln 290	Phe	Asp	Pro	Lys	Thr 295	Gly	Glu	Val	Lys					
_	(2)	INFO	RMAT	ION	FOR	SEQ	ID N	0:52	14:								
10		(i)	(B (C	) LEI ) TY: ) STI	NGTH PE: RAND:	: 17 amin EDNE	TERI: 8 am: 0 ac: SS: :	ino a id sing:	acid:	5							
15		(ii)	MOL	ECUL	E TY	PE: ]	prot	ein									
		(xi)	SEQ	JENCI	E DE	SCRI	PTIO	N: SI	EQ II	ON C	:521	1:					
20		Leu 1	Asn	Lys	Cys	<b>Lys</b> 5	Ile	Ile	Ile	Trp	Arg 10	Ile	Ile	Asn	Met	Lys 15	Asn
25		Lys	Leu	Ile	Ala 20	Lys	Ser	Leu	Leu	Thr 25	Leu	Ala	Ala	Ile	Gly 30	Ile	Thr
23		Thr	Thr	Thr 35	Ile	Ala	Ser	Thr	Ala 40	Asp	Ala	Ser	Glu	Gly 45	Tyr	Gly	Pro
30		Arg	Glu 50	Lys	Lys	Pro	Val	Ser 55	Ile	Asn	His	Asn	Ile 60	Val	Glu	Tyr	Asn
		Asp 65	Gly	Thr	Phe	Lys	Tyr 70	Gln	Ser	Arg	Pro	Lys 75	Phe	Asn	Ser	Thr	Pro 80
35		Lys	Tyr	Ile	Lys	Phe 85	Lys	His	Asp	Tyr	Asn 90	Ile	Leu	Glu	Phe	Asn 95	Asp
		Gly	Thr	Phe	Glu 100	Tyr	Gly	Ala	Arg	Pro 105	Gln	Phe	Asn	Lys	Pro 110	Ala	Ala
40		Lys	Thr	Asp 115	Ala	Thr	Ile	Lys	Lys 120	Glu	Gln	Lys	Leu	Ile 125	Gln	Ala	Gln
45		Asn	Leu 130	Val	Arg	Glu	Phe	Glu 135	Lys	Thr	His	Thr	Val 140	Ser	Ala	His	Arg
45		Lys 145	Ala	Gln	Lys	Ala	<b>Val</b> 150	Asn	Leu	Val	Ser	Phe 155	Glu	Tyr	Lys	Val	Lys 160
50		Lys	Met	Val	Leu	Gln 165	Glu	Arg	Ile	Asp	<b>Asn</b> 170	Val	Leu	Lys	Gln	Gly 175	Leu
		Val	Lys														

(2) INFORMATION FOR SEQ ID NO:5215:

55

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5		(ii)	MOLI	ECULI	E TY	PE: I	prot	ein									
10		(xi)	SEQ	UENCI	E DES	SCRII	PTIO	N: S1	EQ II	ON C	: 521	5 :					
		Lys 1	Glu	Arg	Val	Leu 5	Met	Lys	Lys	Leu	Leu 10	Thr	Ala	Ser	Ile	Ile 15	Ala
15		Cys	Ser	Val	Val 20	Met	Gly	Val	Gly	Leu 25	Val	Asn	Thr	Ser	Ala 30	Glu	Ala
		Ala	Ser	Gly 35	Asn	Ser	Ile	Asp	Thr 40	Val	Lys	Gln	Leu	Ile 45	Lys	Gly	Asp
20		Gln	Ser 50	Leu	Glu	Asn	Val	Lys 55	Ile	Gly	Glu	Ser	Ile 60	Lys	Asp	Val	Leu
		Thr 65	Lys	Tyr	Lys	Asn	Pro 70	Met	Tyr	Ser	Tyr	Asn 75	Glu	Asp	Gly	Thr	Glu 80
25		His	Tyr	Tyr	Glu	Phe 85	His	Thr	Lys	Lys	Gly 90	Met	Leu	Leu	Val	Thr 95	Thr
30		Asp	Gly	Lys	Lys 100	Asn	Asn	Gly	Lys	Val 105	Thr	His	Ile	Ser	Met 110	Met	Tyr
		Asn	Asp	Ala 115	Asn	Gly	Pro	Thr	Tyr 120	Gln	Ala	Val	Lys	<b>As</b> n 125	Tyr	Val	Gly
35		Lys	Ala 130	Val	Thr	His	Thr	Glu 135	Tyr	Ser	Lys	Val	Ala 140	Gly	Asn	Phe	Gly
		Tyr 145	Ile	Glu	Lys	Gly	Lys 150	Thr	Thr	Tyr	Gln	Phe 155	Ala	Ser	Ala	Pro	Lys 160
40		Asp	Lys	Asn	Ile	Lys 165	Leu	Tyr	Arg	Ile	Asp 170	Leu	Glu	Lys			
	(2)	INFO	RMAT:	ION 1	FOR :	SEQ :	ID N	0:52	16:								
45		(i)	(A) (B) (C)	) LEI ) TY: ) STI	NGTH PE: 6 RAND	: 16° amino EDNES	7 am:	sing:	acid	5							
50		(ii)	MOL	ECUL	E TY	PE: ]	prot	ein									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

		1				5					10					15	
5		Asn	Glu	Asp	Gly 20	Ser	Lys	Lys	Lys	Met 25	Ser	Thr	Thr	Ala	Lys 30	Val	Val
		Ser	Ile	Ala 35	Thr	Val	Leu	Leu	Leu 40	Leu	Gly	Gly	Leu	Val 45	Phe	Ala	Ile
10		Phe	Ala 50	Tyr	Val	Asp	His	Ser 55	Asn	Lys	Ala	Lys	Glu 60	Arg	Met	Leu	Asn
		Glu 65	Gln	Lys	Gln	Glu	Gln 70	Lys	Glu	Lys	Arg	Gln 75	Lys	Glu	Asn	Ala	Glu 80
15		Lys	Glu	Arg	Lys	Lys 85	Lys	Gln	Gln	Glu	Glu 90	Lys	Glu	Gln	Asn	Glu 95	Leu
		Asp	Ser	Gln	Ala 100	Asn	Gln	Tyr	Gln	Gln 105	Leu	Pro	Gln	Gln	Asn 110	Gln	Tyr
20		Gln	Tyr	Val 115	Pro	Pro	Gln	Gln	Gln 120	Ala	Pro	Thr	Lys	Gln 125	Arg	Pro	Ala
25		Lys	Glu 130	Glu	Asn	Asp	Asp	Lys 135	Ala	Ser	Lys	Asp	Glu 140	Ser	Lys	Asp	Lys
25		<b>As</b> p 145	Asp	Lys	Ala	Ser	Gln 150	Asp	Lys	Ser	Asp	<b>A</b> sp 155	Asn	Gln	Lys	Lys	Thr 160
30		Asp	Asp	Asn	Lys	Gln 165	Pro	Ala									
	(2)	INFO	TAMS	ON I	FOR S	SEQ I	D NO	0:521	17:								
35		(i)	(B)	LEN TYP STP	NGTH:	115 mino EDNES	ami aci	ino a id singl	acida	5							
40		(ii)	MOLE	ECULE	E TYE	E: p	rote	ein									
45		(xi)	SEQU	JENCE	E DES	SCRIE	PTION	1: SE	EQ II	NO:	5217	7:					
43		Met 1	Lys	Arg	Asn	Phe 5	Pro	Lys	Leu	Ile	Ala 10	Leu	Ser	Leu	Ile	Phe 15	Ser
50		Leu	Ser	Val	Thr 20	Pro	Ile	Ala	Asn	Ala 25	Glu	Ser	Asn	Ser	Asn 30	Ile	Lys
		Ala	Lys	Asp 35	Lys	Lys	His	Val	Gln 40	Val	Asn	Val	Glu	Asp 45	Lys	Ser	Val
55		Pro	Thr 50	Asp	Val	Arg	Asn	Leu 55	Ala	Gln	Lys	Asp	Tyr 60	Leu	Ser	Tyr	Val

		65					70					75					80
5		Gly	Glu	Pro	Phe	Lys 85	Ile	Tyr	Lys	Phe	Asn 90	Lys	Lys	Ser	Asp	Gly 95	Asn
		Tyr	Tyr	Phe	Pro 100	Val	Leu	Asn	Thr	Glu 105	Gly	Asn	Ile	Asp	Tyr 110	Ile	Val
10		Thr	Ile	Ser 115													
	(2)	INFOR	TAMS	ON I	FOR S	SEQ I	ID NO	521	L8:								
15		(i)	(B) (C)	LEN TYI STI	NGTH:	: 173 amino EDNES	3 am: 5 ac: 55: 8	ino a id singl	acida	3							
20		(ii)	MOL	ECULI	E TYP	PE: I	prote	ein									
25		(xi)	SEQU	JENCI	E DES	SCRII	PTIO	1: SI	EQ II	ONO:	:5218	3:					
		Asn 1	Phe	Lys	Met	Gln 5	Glu	Val	Lys	Tyr	Met 10	Thr	Glu	Ile	Thr	Phe 15	Lys
30		Gly	Gly	Pro	Ile 20	His	Leu	Lys	Gly	Gln 25	Gln	Ile	Asn	Glu	Gly 30	Asp	Phe
		Ala	Pro	Asp 35	Phe	Thr	Val	Leu	Asp 40	Asn	Asp	Leu	Asn	Gln 45	Val	Thr	Leu
35		Ala	Asp 50	Туг	Ala	Gly	ГЛЗ	Lys 55	Lys	Leu	Ile	Ser	Val 60	Val	Pro	Ser	Ile
		Asp 65	Thr	Gly	Val	Cys	Asp 70	Gln	Gln	Thr	Arg	Lys 75	Phe	Asn	Ser	Asp	Ala 80
40		Ser	Lys	Glu	Glu	Gly 85	Ile	Val	Leu	Thr	Ile 90	Ser	Ala	Asp	Leu	Pro 95	Phe
		Ala	Gln	Lys	Arg 100	Trp	Cys	Ala	Ser	Ala 105	Gly	Leu	Asp	Asn	Val 110	Ile	Thr
45		Leu	Ser	Asp 115	His	Arg	Asp	Leu	Ser 120	Phe	Gly	Glu	Asn	Tyr 125	Gly	Val	Val
50		Met	Glu 130	Glu	Leu	Arg	Leu	Leu 135	Ala	Arg	Ala	Val	Phe 140	Val	Leu	Asp	Ala
		Asp 145	Asn	Lys	Val	Val	Tyr 150	Lys	Glu	Ile	Val	<b>Se</b> r 155	Glu	Gly	Thr	Asp	Phe 160
55		Pro	Asp	Phe	Asp	Ala 165		Leu	Ala	Ala	Tyr 170	Lys	Asn	Ile			

5		(i)	(B (C	UENCI ) LEI ) TYI ) STI ) TOI	NGTH PE: 8 RAND	: 139 amino EDNES	9 am: 0 ac: 55: 3	ino i id sing	acid	<b>S</b>							
		(ii)	MOL	ECULI	E TY	PE: 1	prote	ein									
10																	
		(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: 51	EQ II	ON C	:521	9:					
15		Ile 1	Glu	Ser	Arg	Phe 5	Ile	Met	Ala	Lys	Ile 10	Asn	Phe	Asp	Ala	Ala 15	Thr
		Lys	Gly	Asn	Pro 20	Gly	Ile	Ser	Thr	Cys 25	Ala	Ile	Val	Ile	Lys	Glu	Asp
20		Glu	Gln	His 35	Tyr	Thr	Tyr	Thr	His 40	Glu	Leu	Gly	Glu	Met 45	Asp	Asn	His
		Thr	Ala 50	Glu	Trp	Ala	Ala	Cys 55	Ile	Tyr	Ala	Leu	Glu 60	His	Ala	Arg	Glu
25		Leu 65	Asn	Val	Gln	Asn	Ala 70	Leu	Leu	Tyr	Thr	<b>Asp</b> 75	Ser	Lys	Leu	Ile	Ala 80
30		Asp	Ser	Ile	Glu	Ala 85	Gly	Tyr	Val	Lys	Asn 90	Ala	Asn	Phe	Lys	Pro 95	Tyr
		Phe	Asp	Gln	Ile 100	Glu	Ile	Phe	Glu	Lys 105	Asp	Phe	Asp	Leu	Leu 110	Phe	Val
35		Lys	Trp	Ile 115	Pro	Arg	Glu	Gln	Asn 120	Lys	Glu	Ala	Asn	Gln 125	His	Ala	Gln
		Gln	Ala 130	Leu	Tyr	Lys	Leu	Ile 135	Lys	Lys	Asn	Lys					
40	(2)	INFO	RMAT:	ION I	FOR S	SEQ I	ID NO	D: 52	20:								
45		(i)	(B)	UENCI LEI TYI STI	NGTH PE: 3 RANDI	: 162 amino EDNES	2 am: 5 ac: 5S: 8	ino a id sing:	acid	3							
		(ii)															
50																	
		(xi)	SEQ	JENCI	E DES	SCRII	PTIO	N: S	EQ II	ON C	: 522	0:					
55		Met 1	Pro	Gly	Thr	Val 5	Leu	Asp	Pro	Gln	Met 10	Ile	Lys	Asn	Glu	Asp 15	Val

20 25 30 Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp 5 Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn 10 Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys 15 Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu 20 Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile 25 Met Gln (2) INFORMATION FOR SEQ ID NO:5221: 30 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 35 (ii) MOLECULE TYPE: protein 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221: Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu 45 Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu

Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys

Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg

70

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						85					90					95	
5		Asp	Arg	Arg	Ile 100	Glu	Ile	Asp	Ile	Lys 105	Ser	Lys	Asp	Glu	Ile 110	Gly	Asp
		Thr	Ile	Tyr 115	Arg	Thr	Val	Ile	Leu 120	Glu	Ile	Met	Gly	Lys 125	His	Ser	Asn
10		Leu	Ile 130	Leu	Val	Asp	Glu	Asn 135	Arg	Lys	Ile	Ile	Glu 140	Gly	Phe	Lys	His
		Leu 145	Thr	Pro	Asn	Thr	Asn 150	His	Tyr	Arg	Thr	Val 155	Met	Pro	Gly	Phe	Asn 160
15		Tyr	Glu	Ala	Pro	Pro 165	Thr	Gln	His	Lys	Ile 170	Asn	Pro	Tyr	Asp	Ile 175	Thr
		Gly	Ala	Glu	Val 180	Leu	Lys	Tyr	Ile	Asp 185	Phe	Asn	Ala	Gly	Asn 190	Ile	Ala
20		Lys	Gln	Leu 195	Leu	Asn	Gln	Phe	Glu 200	Gly	Phe	Ser	Pro	Leu 205	Ile	Thr	Asn
25		Glu	Ile 210	Val	Ser	Arg	Arg	Gln 215	Phe	Met	Thr	Ser	Ser 220	Thr	Leu	Pro	Glu
25		Ala 225	Phe	Asp	Glu	Val	Met 230	Ala	Glu	Thr	Lys	Leu 235	Pro	Pro	Thr	Pro	Ile 240
30		Phe	His	Lys	Asn	His 245	Glu	Thr	Gly	Lys	Glu 250	Asp	Phe	Tyr	Phe	Ile 255	Lys
		Leu	Asn	Gln	Phe 260	Asn	Asp	Asp	Thr	Val 265	Thr	Tyr	Asp	Ser	Leu 270	Asn	Asp
35		Leu	Leu	Asp 275	Arg	Phe	Tyr	Asp	Ala 280	Arg	Gly	Glu	Arg	Glu 285	Arg	Val	Lys
		Gln	Arg 290		Asn	Asp	Leu			Phe				Gln	Leu	His	Lys
40		Tyr 305	Gln	Asn	Lys	Leu	Ala 310	Ser									
	(2)	INFOR	ITAMS	ON F	FOR S	EQ I	D NC	: 522	2:								
45		(i)		JENCE				TICS	ۇ: -دىنى								

- (A) LENGTH: 245 amino acids(B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

		1				5					10					15	
5		Glu	Gln	Leu	Tyr 20	Gly	Glu	Leu	Ile	Thr 25	Ala	Asn	Ile	Tyr	Arg 30	Ile	Lys
		Gln	Gly	Asp 35	Lys	Glu	Val	Thr	Ala 40	Leu	Asn	Tyr	Tyr	Thr 45	Asn	Glu	Glu
10		Val	Val 50	Ile	Pro	Leu	Asn	Pro 55	Thr	Lys	Ser	Pro	Ser 60	Ala	Asn	Ala	Gln
		Tyr 65	Tyr	Tyr	Lys	Gln	Tyr 70	Xaa	Arg	Met	Lys	Thr 75	Arg	Xaa	Arg	Glu	Leu 80
15		Gln	His	Gln	Ile	Gln 85	Leu	Thr	Lys	Asp	Asn 90	Ile	Asp	Tyr	Phe	Ser 95	Thr
20		Ile	Glu	Gln	Gln 100	Leu	His	His	Ile	Ser 105	Val	His	Asp	Ile	Asp 110	Glu	Ile
		Arg	Asp	Glu 115	Leu	Ala	Glu	Gln	Gly 120	Phe	Met	Lys	Gln	Arg 125	Lys	Asn	Gln
25		Thr	Lys 130	Lys	Lys	Lys	Ala	Gln 135	Ile	Gln	Leu	Gln	His 140	Tyr	Val	Ser	Thr
		Asp 145	Gly	Asp	Asp	Ile	Tyr 150	Val	Gly	Lys	Asn	Asn 155	Lys	Gln	Asn	Asp	Tyr 160
30		Leu	Thr	Asn	Lys	Lys 165	Ala	Lys	Lys	Thr	His 170	Thr	Trp	Leu	His	Thr 175	Lys
35		Asp	Ile	Pro	Gly 180	Ser	His	Val	Val	Ile 185	Phe	Asn	Asp	Ala	Pro 190	Ser	Asp
,,		Thr	Thr	Ile 195	Lys	Glu	Ala	Ala	Met 200	Leu	Ala	Gly	Tyr	Phe 205	Ser	Lys	Ala
10		Gly	Asn 210	Ser	Gly	Gln	Ile	Pro 215	Val	Asp	Tyr	Thr	Leu 220	Ile	Lys	Asn	Val
		His 225	Lys	Pro	Ser	Gly	Ala 230	Lys	Pro	Gly	Phe	Val 235	Thr	Tyr	Asp	Asn	Gln 240
45		Lys	Thr	Leu	Tyr	Ala 245											
	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID NO	D: <b>52</b> 2	23:								
50		(i)	(A) (B) (C)	LEN TYP	NGTH PE: 8 RANDI	ARACT : 99 amino EDNES	amin o aci	no ad id singl	cids								
55		(ii)	MOLI	ECULI	E TYI	PE: J	prote	ein									

	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	: 522	3:					
5	Tyr 1	Ile	Thr	Asn	Pro 5	Gln	Asn	Pro	Lys	Ile 10	Lys	Ile	Thr	Gly	Ile 15	Ser
	Leu	Ser	Ser	Gly 20	Val	Gly	Asn	Phe	Phe 25	Ile	Ile	Thr	Asn	Gly 30	Lys	Arg
10	Ile	Ile	Val 35	Ala	Lys	Ile	Lys	Arg 40	Asn	Ala	Asp	Asn	Asp 45	Ser	Ala	Leu
	Lys	Ser 50	Phe	Asn	Ala	Ile	Phe 55	Ile	Ile	Gly	Asn	Ala 60	Asp	Pro	His	Asn
15	<b>Me</b> t 65	Ile	Val	Asn	Lys	Tyr 70	Asp	Arg	Lys	Val	Val 75	Ser	Arg	Ser	Leu	Phe 80
20	· Ile	Asn	Ile	Ile	Thr 85	Pro	Leu	Ile	Met	Суз 90	Phe	Tyr	Ile	Lys	Lys 95	Tyr
20	Asp	Leu	Lys													
	(2) INFO	RMAT:	ION I	FOR S	SEQ I	D NO	522	24:								
?5	(i)	(B)	LEI TYI	E CHA NGTH: PE: & RANDE POLOC	: 131 amino EDNES	Lami Saci	ino a id singl	cids	3							
30	(ii)															
35	(xi)	SEQU	JENCI	E DES	SCRIE	PTION	I: SE	Q II	ONO:	5224	i:					
	Glu 1	Asn	Val	Leu	Ala 5	Lys	Glu	Tyr	Ala	Val 10	Lys	Tyr	Asn		Val 15	Glu
40	Ala	Ile	Gln	His 20	Arg	Gly	Glu	Thr	Val 25	Thr	Glu	Gly	Ser	Ser 30	Ser	Asn
45	Ala	Tyr	Ala 35	Ile	Lys	Asp	Gly	Val 40	Ile	Tyr	Thr	His	Pro 45	Ile	Asn	Asn
	Tyr	Ile 50	Leu	Asn	Gly	Ile	Thr 55	Arg	Ile	Val	Ile	Lys 60	Lys	Ile	Ala	Glu
50	Asp 65	Tyr	Asn	Ile	Pro	Phe 70	Lys	Glu	Glu	Thr	Phe 75	Thr	Val	Asp	Phe	Leu 80
	Lys	Asn	Ala	Asp	Glu 85	Val	Ile	Val	Ser	Ser 90	Thr	Ser	Ala	Glu	Val 95	Thr
55	Pro	Val	Ile	Lys 100	Leu	Asp	Gly	Glu	Pro 105	Val	Asn	Asp	Gly	Lys 110	Val	Gly

				115					120					125			
5		His	Ser 130	Ile													
	(2)	INFO	RMAT	ON E	FOR S	SEQ I	D NO	:522	25 :								
10		(i)	(B)	JENCE LEN TYPE STE TOP	NGTH: PE: 8 RANDI	540 mino EDNES	ami aci SS: s	ino a id singl	acids	;							
15		(ii)	MOLI	ECULE	TYI	E: r	rote	ein									
		(xi)	SEQU	JENCE	E DES	CRI	OIT	1: SE	EQ II	NO:	5225	S:					
20		Asn 1	His	Leu	Thr	Ala 5	Arg	Ile	Ile	Asn	Gln 10	Glu	Asp	Asp	Leu	Met 15	Asn
25		Leu	Phe	Arg	Gln 20	Gln	Lys	Phe	Ser	Ile 25	Arg	Lys	Phe	Asn	Val 30	Gly	Ile
		Phe	Ser	Ala 35	Leu	Ile	Ala	Thr	Val 40	Thr	Phe	Ile	Ser	Thr 45	Asn	Pro	Thr
30		Thr	Ala 50	Ser	Ala	Ala	Glu	Gln 55	Asn	Gln	Pro	Ala	Gln 60	Asn	Gln	Pro	Ala
		Gln 65	Pro	Ala	Asp	Ala	Asn 70	Thr	Gln	Pro	Asn	<b>Ala</b> 75	Asn	Ala	Gly	Ala	Gln 80
35		Ala	Asn	Pro	Thr	Ala 85	Gln	Pro	Ala	Ala	Pro 90	Ala	Asn	Gln	Gly	Gln 95	Pro
		Ala	Val	Gln	Pro 100	Ala	Asn	Gln	Gly	Gly 105	Gln	Ala	Asn	Pro	Ala 110	-	Gly
40		Ala	Ala	Gln 115	Pro	Asn	Thr	Gln	Pro 120	Ala	Gly	Gln	Gly	Asp 125	Gln	Ala	Asp
45		Pro	Asn 130	Asn	Ala	Ala	Gln	Ala 135	Gln	Pro	Gly	Asn	Gln 140	Ala	Thr	Pro	Ala
70		Asn 145	Gln	Ala	Gly	Gln	Gly 150	Asn	Asn	Gln	Ala	Thr 155	Pro	Asn	Asn	Asn	Ala 160
50		Thr	Pro	Ala	Asn	Gln 165	Thr	Gln	Pro	Ala	Asn 170	Ala	Pro	Ala	Ala	Ala 175	Gln
		Pro	Ala	Ala	Pro 180	Val	Ala	Ala	Asn	Ala 185	Gln	Thr	Gln	Asp	Pro 190	Asn	Ala
55		Ser	Asn	Thr 195	Gly	Glu	Gly	Ser	Ile 200	Asn	Thr	Thr	Leu	Thr 205	Phe	Asp	Asp

210 215 220 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly 235 5 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val 10 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr 15 295 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp 315 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu 345 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly 30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro 395 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn 35 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr 455 45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly 465 Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp 50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser

520

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530 535 540 (2) INFORMATION FOR SEQ ID NO:5226: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 177 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: protein 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226: Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val 20 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile 25 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe 30 Phe Phe Ile Ile Thr Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu 35 100 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro 40 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile 45 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val 170 Lys 50 (2) INFORMATION FOR SEQ ID NO:5227: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(C) STRANDEDNESS: single

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(ii) MOLECULE TYPE: protein

5	(x	i)	SEOU	JENCI	E DE:	SCRI	PTIO	N: SI	EO II	O NO	. 522	7 -					
													Gly	Glu	Phe	Asn 15	Ala
10	T	hr	Gly	Thr	Lys 20	Leu	Leu	Tyr	Asn	Lys 25	Pro	Ile	Gln	Gln	Gln 30	Leu	Gln
15	н	is	Ile	Thr 35	Tyr	Ile	Pro	Gln	Lys 40	Ala	His	Ile	Asp	Leu 45	Asp	Phe	Pro
	I	le	Ser 50	Val	Glu	Gln	Val	Ile 55	Leu	Ser	Gly	Cys	Tyr 60	Lys	Glu	Ile	Gly
20	T: 6:		Phe	Arg	Arg	Pro	Asn 70	Lys	Ser	Ala	Arg	Asp 75	Lys	Leu	Lys	Gln	Leu 80
	L	eu	Ser	Asp	Leu	Glu 85	Leu	Glu	Ser	Leu	Arg 90	His	Arg	Gln	Ile	Ser 95	Glu
25	Le	eu	Ser	Gly	Gly 100	Gln	Leu	Gln	Arg	<b>Val</b> 105	Leu	Val	Ala	Arg	Ala 110	Leu	Met
30	Se	er	Xaa	Ser 115	Glu	Val	Tyr	Phe	Leu 120	Asp	Glu	Pro	Phe	<b>Val</b> 125	Gly	Ile	Asp
	Pl	he	Ser 130	Ser	Glu	Lys	Leu	Ile 135	Met	Thr	Lys	Ile	Glu 140	Asn	Leu	Lys	Gln
35		ln 45	Gly	Lys	Leu	Ile	Leu 150	Ile	Ile	His	His	Asp 155	Leu	Ser	Lys	Ala	Lys 160
	G.	ln	Tyr	Phe	Asp	Arg 165	Ile	Ile	Leu	Leu	Asn 170	Gln	Thr	Leu	Arg	Tyr 175	Phe
40	G:	ly	Asp	Ser	Glu 180	Glu	Ala	Met	Ser	Val 185	Thr	Arg	Leu	Asn	Glu 190	Thr	Phe
	Me	et	Ser	Ser 195	Thr	Asp	Сув	Ser	Asp 200	Pro	Ser	Gln	Arg	Ser 205	Asn	Ile	Thr
45	C)	ys															
	(2) IN	FOR	ITAM	ON F	FOR S	SEQ 1	ID NO	522	28:								
50	(:	i)	(A) (B) (C)	LEN TYP STF	IGTH: PE: 8 KANDI	: 256 mino EDNES	TERIS  ami  aci  SS: s  line	ino a id singl	acids	5							

	(xi)	SEQ	JENCE	E DES	SCRI	OITS	N: SI	II QE	NO:	5228	3:					
5	Thr 1	Phe	Arg	Ile	Ile 5	Phe	Leu	Leu	Ser	Ile 10	Arg	Lys	Arg	Ser	Asn 15	Arg
	Thr	His	Val	Ser 20	Ile	His	Trp	Ser	Thr 25	Val	Asn	Lys	Glu	Glu 30	Ile	Cys
10	Leu	Arg	Val 35	Lys	Asp	Asn	Leu	Gln 40	Gln	Ile	Ser	Thr	Gln 45	Ile	Asn	Asp
	Lys	Ser 50	Glu	Lys	Asn	Asn	Phe 55	Ser	Thr	Lys	Pro	Asn 60	Val	Ile	Ala	Val
15	Thr 65	Lys	Tyr	Val	Thr	Ile 70	Glu	Arg	Ala	Lys	Glu 75	Ala	Tyr	Glu	Ala	Gly 80
20	Ile	Arg	His	Phe	Gly 85	Glu	Asn	Arg	Leu	Glu 90	Gly	Phe	Phe	Gln	Lys 95	Lys
	Glu	Ala	Leu	Pro 100	Ser	Asp	Ala	Val	Ile 105	His	Phe	Ile	Gly	Ser 110	Leu	Gln
25	Ser	Arg	Lys 115	Val	Lys	Asp	Val	Ile 120	Asn	Asp	Val	Asp	Tyr 125	Phe	His	Ala
	Leu	Asp 130	Arg	Leu	Ser	Leu	Ala 135	Lys	Glu	Ile	Asn	Lys 140	Arg	Ala	Glu	His
30	Lys 145	Ile	Lys	Cys	Phe	Leu 150	Gln	Val	Asn	Val	Ser 155	Gly	Glu	Ala	Ser	Lys 160
	His	Gly	Ile	Ala	Leu 165	Glu	Asp	Val	Asp	Gln 170	Phe	Ile	Asp	Asp	Leu 175	Lys
35	Lys	Tyr	Asp	Lys 180	Ile	Glu	Ile	Val	Gly 185	Leu	Met	Thr	Met	Ala 190		Leu
40	Thr	Asp	<b>As</b> p 195	Glu	Ala	Tyr	Ile	<b>Ar</b> g 200	Ser	Leu	Phe	Lys	Gln 205	Leu	Arg	Leu
	Lys	Lys 210	Glu	Glu	Ile	Gln	Arg 215	Leu	Asn	Leu	Glu	Tyr 220	Ala	Pro	Cys	Asp
45	Glu 225	Leu	Ser	Met	Gly	Met 230	Ser	Asn	Asp	Tyr	Leu 235	Ile	Ala	Val	Glu	Glu 240
	Gly	Ala	Thr	Phe	Val 245	Arg	Ile	Gly	Thr	Lys 250	Leu	Val	Gly	Glu	Glu 255	Glu
50																

(2) INFORMATION FOR SEQ ID NO:5229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 246 amino acids
    (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:5230:

5																
	(xi)	SEQ	UENC	E DE:	SCRI	PTIO	N: S1	EQ II	ON C	:522	9:					
10	Lys 1	His	Lys	Leu	Thr 5	Ile	Ile	Thr	Gly	Gly 10	Phe	Phe	Thr	Met	Lys 15	Lys
	Thr	Ile	Met	Ala 20	Ser	Ser	Leu	Ala	Val 25	Ala	Leu	Gly	Val	Thr 30	Gly	Туг
15	Ala	Ala	Gly 35	Thr	Gly	His	Gln	Ala 40	His	Ala	Ala	Glu	Val 45	Asn	Val	Asp
20	Gln	Ala 50	His	Leu	Val	Asp	Leu 55	Ala	His	Asn	His	Gln 60	Asp	Gln	Leu	Asn
	Ala 65	Ala	Pro	Ile	Lys	Asp 70	Gly	Ala	Tyr	Asp	Ile 75	His	Phe	Val	Lys	Asp 80
25	Gly	Phe	Gln	Tyr	Asn 85	Phe	Thr	Ser	Asn	Gly 90	Thr	Thr	Trp	Ser	Trp 95	Ser
	Tyr	Glu	Ala	Ala 100	Asn	Gly	Gln	Thr	Ala 105	Gly	Phe	Ser	Asn	<b>Val</b> 110	Ala	Gly
30	Ala	Asp	Tyr 115	Thr	Thr	Ser	Tyr	Asn 120	Gln	Gly	Ser	Asn	Val 125	Gln	Ser	Val
	Ser	Tyr 130	Asn	Ala	Gln	Ser	Ser 135	Asn	Ser	Asn	Val	Glu 140	Ala	Val	Ser	Ala
35	Pro 145	Thr	Tyr	His	Asn	Tyr 150	Ser	Thr	Ser	Thr	Thr 155	Ser	Ser	Ser	Val	Arg 160
40	Leu	Ser	Asn	Gly	<b>As</b> n 165	Thr	Ala	Gly	Ala	Thr 170	Gly	Ser	Ser	Ala	Ala 175	Gln
40	Ile	Met	Ala	Gln 180	Arg	Thr	Gly	Val	Ser 185	Ala	Ser	Thr	Trp	Ala 190	Ala	Ile
45	Ile	Ala	Arg 195	Glu	Ser	Asn	Gly	Gln 200	Val	Asn	Ala	Tyr	Asn 205	Pro	Ser	Gly
	Ala	Ser 210	Gly	Leu	Phe	Gln	Thr 215	Met	Pro	Gly	Trp	Gly 220	Pro	Thr	Asn	Thr
50	Val 225	Asp	Gln	Gln	Ile	Asn 230	Ala	Ala	Val	Lys	Ala 235	Tyr	Lys	Ala	Gln	Gly 240
	Leu	Gly	Ala	Trp	Gly 245	Phe										

(A) LENGTH: 519 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

	(ii)	MOL	ECULI	E TYI	PE: p	prote	ein									
10	(xi)	SEQU	JENCI	E DES	SCRII	PTIO	N: SI	EQ II	NO:	: 523(	) :					
	Lys 1	Glu	Pro	His	Lys 5	Met	Lys	Lys	Ile	Tyr 10	Lys	Ser	Leu	Thr	Val 15	Ser
15	Ala	Ile	Val	Ala 20	Thr	Val	Ser	Leu	Ser 25	Ala	Leu	Pro	Gln	Ser 30	Leu	Ala
20	Ile	Thr	His 35	Glu	Ser	Gln	Pro	Thr 40	Lys	Gln	Gln	Arg	Thr 45	Val	Leu	Ph∈
20	Aap	Arg 50	Ser	His	Gly	Gln	Thr 55	Ala	Gly	Ala	Ala	Asp 60	Trp	Val	Ser	Asp
25	Gly 65	Ala	Phe	Ser	Asp	Tyr 70	Ala	Asp	Ser	Ile	Gln 75	Lys	Gln	Gly	Tyr	Asp 80
	Val	Lys	Ala	Ile	Asp 85	Gly	His	Ser	Asn	Ile 90	Thr	Glu	Ala	Ser	Leu 95	Lys
30	Ser	Ser	Lys	Ile 100	Phe	Val	Ile	Pro	Glu 105	Ala	Asn	Ile	Pro	Phe 110	Lys	Glu
	Ser	Glu	Gln 115	Ala	Ala	Ile	Val	Lys 120	Tyr	Val	Lys	Gln	Gly 125	Gly	Asn	Val
35	Val	Phe 130	Ile	Ser	Asp	His	Tyr 135	Asn	Ala	Asp	Arg	Asn 140	Leu	Asn	Arg	Ile
	Asp 145	Ser	Ser	Glu	Ala	Met 150	Asn	Gly	Tyr	Arg	Arg 155	Gly	Ala	Tyr.	Glu	Asp 160
40	Met	Ser	Lys	Gly	Met 165	Asn	Ala	Glu	Glu	Lys 170	Ser	Ser	Thr	Ala	Met 175	Glr
45	Gly	Val	Lys	Ser 180	Ser	Asp	Trp	Leu	<b>Ser</b> 185	Thr	Asn	Phe	Gly	<b>Val</b> 190	Arg	Phe
	Arg	Tyr	Asn 195	Ala	Leu	Gly	Asp	<b>Leu</b> 200	Asn	Thr	Ser	Asn	11e 205	Val	Ser	Ser
50	Lys	Glu 210	Ser	Phe	Gly	Ile	Thr 215	Glu	Gly	Val	Lys	Ser 220	Val	Ser	Met	His
	Ala 225	Gly	Ser	Thr	Leu	Ala 230	Ile	Thr	Asn	Pro	Glu 235	Lys	Ala	Lys	Gly	Ile 240
55	Val	Tyr	Thr	Pro	Glu 245	Gln	Leu	Pro	Ala	Lys 250	Ser	Lys	Trp	Ser	His 255	Ala

		Val	Asp	Gln	Gly 260	Ile	Tyr	Asn	Gly	Gly 265	Gly	Lys	Ala	Glu	Gly 270	Pro	Tyr
5		Val	Ala	Ile 275	Ser	Lys	Val	Gly	Lys 280	Gly	Lys	Ala	Ala	Phe 285	Ile	Gly	Asp
		Ser	Ser 290	Leu	Val	Glu	Asp	Ser 295	Ser	Pro	Lys	Tyr	Val 300	Arg	Glu	Asp	Asn
10		Gly 305	Glu	Lys	Lys	Lys	Thr 310	Tyr	Asp	Gly	Phe	Lys 315	Glu	Gln	Asp	Asn	Gly 320
15		Lys	Leu	Leu	Asn	<b>Asn</b> 325	Ile	Thr	Ala	Trp	Met 330	Ser	Lys	Asp	<b>As</b> n	Asp 335	Gly
		Lys	Ser	Leu	Lys 340	Ala	Ser	Ser	Leu	Thr 345	Leu	Asp	Thr	Lys	Thr 350	Lys	Leu
20		Leu	Asp	Phe 355	Glu	Arg	Pro	Glu	Arg 360	Ser	Thr	Glu	Pro	Glu 365	Lys	Glu	Pro
		Trp	Ser 370	Gln	Pro	Pro	Ser	Gly 375	Tyr	Lys	Trp	Tyr	Asp 380	Pro	Thr	Thr	Phe
25		Lys 385	Ala	Gly	Ser	Tyr	Gly 390	Ser	Glu	Lys	Gly	Ala 395	Asp	Pro	Gln	Pro	<b>Asn</b> 400
		Thr	Pro	Asp	Asp	His 405	Thr	Pro	Pro	Asn	Gln 410	Asn	Glu	Lys	Val	Thr 415	Phe
30		Asp	Ile	Pro	Gln 420	Asn	Val	Ser	Val	Asn 425	Glu	Pro	Phe	Glu	Met 430	Thr	Ile
35		His	Leu	Lys 435	Gly	Phe	Glu	Ala	Asn 440	Gln	Thr	Leu	Glu	Asn 445	Leu	Arg	Val
		Gly	Ile 450	Tyr	Lys	Glu	Gly	Gly 455	Arg	Gln	Ile	Gly	Gln 460	Phe	Ser	Ser	Lys
40		Asp 465	Asn	Asp	Tyr	Asn	Pro 470	Pro	Gly	Tyr	Ser	Thr 475		Pro	Thr		Lys 480
		Ala	Asp	Glu	Asn	Gly 485	Asn	Val	Thr	Ile	Lys 490	Val	Asn	Ala	ГÀЗ	Val 495	Leu
45		Glu	Ser	Met	Glu 500	Gly	Ser	Lys	Ile	Arg 505	Leu	Lys	Leu	Gly	<b>Asp</b> 510	Lys	Thr
		Leu	Ile	Thr 515	Thr	Asp	Phe	Lys									
50	(2)	INFOR	TAMS	ON I	FOR S	SEQ 1	ID NO	523	31:								
		(i)		LEN	E CHA NGTH: PE: 8	316	ami	ino a		3							
55			(C)	ST	RANDE	EDNES	SS: 5	singl	le								

	(xi)	SEQ	JENCI	E DES	SCRI	OITS	1: SI	EQ II	NO:	5233	l:					
5	Arg 1	Asp	Glu	Arg	Ile 5	Lys	Thr	Met	Thr	Asn 10	Ser	Ser	Lys	Ser	Phe 15	Thr
	Lys	Phe	Met	Ala 20	Ala	Ser	Ala	Val	Phe 25	Thr	Met	Gly	Phe	Leu 30	Ser	Va]
10	Pro	Thr	Ala 35	Gly	Ala	Glu	Gln	Thr 40	Asn	Gln	Ile	Ala	Asn 45	Lys	Pro	Glr
	Ala	Ile 50	Gln	Trp	His	Thr	Asn 55	Leu	Thr	Asn	Glu	Arg 60	Phe	Thr	Thr	Ile
15	Ala 65	His	Arg	Gly	Ala	Ser 70	Gly	Tyr	Ala	Pro	Glu 75	His	Thr	Phe	Gln	Ala 80
20	Tyr	Asp	Lys	Ser	His 85	Asn	Glu	Leu	Lys	Ala 90	Ser	Tyr	Ile	Glu	Ile 95	Asp
	Leu	Gln	Arg	Thr 100	Lys	Asp	Gly	His	Leu 105	Val	Ala	Met	His	Asp 110	Glu	Thr
25	Val	Asn	Arg 115	Thr	Thr	Asn	Gly	His 120	Gly	Lys	Val	Glu	Asp 125	Tyr	Thr	Leu
	Asp	Glu 130	Leu	Lys	Gln	Leu	Asp 135	Ala	Gly	Ser	Trp	Phe 140	Asn	Lys	Lys	Туг
30	Pro 145	Lys	Tyr	Ala	Arg	Ala 150	Ser	Tyr	Lys	Asn	Ala 155	Lys	Val	Pro	Thr	Le:
35	Asp	Glu	Ile	Leu	Glu 165	Arg	Tyr	Gly	Pro	<b>As</b> n 170	Ala	Asn	Tyr	Tyr	Ile 175	Glu
	Thr	Lys	Ser	Pro 180	Asp	Val	Tyr	Pro	Gly 185	Met	Glu	Glu	Gln	Leu 190	Leu	Ala
40	Ser	Leu	Lys 195	Lys	His	His	Leu	<b>Leu</b> 200	Asn	Asn	Asn	Lys	Leu 205	Lys	Asn	Gly
	His	Val 210	Met	Ile	Gln	Ser	Phe 215	Ser	Asp	Glu	Ser	Leu 220	Lys	Lys	Ile	His
45	Arg 225	Gln	Asn	Lys	His	Val 230	Pro	Leu	Val	Lys	Leu 235	Val	Asp	Lys	Gly	Glu 240
50	Leu	Gln	Gln	Phe	Asn 245	Asp	Gln	Arg	Leu	Lys 250	Glu	Ile	Arg	Ser	Tyr 255	Ala
	Ile	Gly	Leu	Gly 260	Pro	Asp	Tyr	Thr	Asp 265	Leu	Thr	Glu	Gln	<b>Asn</b> 270	Thr	His
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile 280	Val	His	Pro	Tyr	Thr	Val	Asn	Glu

		Lys	Ala 290	Asp	Met	Leu	Arg	Leu 295	Asn	Lys	Tyr	Gly	<b>Val</b> 300	Asp	Gly	Val	Phe
5		Thr 305	Asn	Phe	Ala	Asp	Lys 310	Tyr	Lys	Glu	Val	Ile 315	Lys				
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10		(i)	(A) (B) (C)	LEN TYI	NGTH: PE: & RANDI	ARACT 433 amino EDNES SY: ]	3 am: cac: SS: s	ino a id sing!	acid	3							
15		(ii)	MOLE	ECULI	E TYI	?E: p	prote	ein									
20		(xi)	SEQU	JENCE	E DES	SCRI	PTIO	1: SI	EQ II	NO:	5232	2 :					
		Arg 1	Phe	Met	Lys	Asn 5	Leu	Ile	Ser	Ile	Ile 10	Ile	Ile	Leu	Cys	Leu 15	Thr
25		Leu	Ser	Ile	Met 20	Thr	Pro	Tyr	Ala	Gln 25	Ala	Thr	Asn	Ser	<b>As</b> p 30	Val	Thr
		Pro	Val	Gln 35	Ala	Ala	Asn	Gln	Tyr 40	Gly	Tyr	Ala	Gly	Leu 45	Ser	Ala	Ala
30		Tyr	Glu 50	Pro	Thr	Ser	Ala	<b>Val</b> 55	Asn	Val	Ser	Gln	Thr 60	Gly	Gln	Leu	Leu
		Tyr 65	Gln	Tyr	Asn	Ile	Asp 70	Thr	Lys	Trp	Asn	Pro 75	Ala	Ser	Met	Thr	Lys 80
35		Leu	Met	Thr	Met	Tyr 85	Leu	Thr	Leu	Glu	Ala 90	Val	Asn	Lys	Gly	Gln 95	Leu
40		Ser	Leu	Asp	Asp 100	Thr	Val	Thr	Met	Thr 105	Asn	Lys	Glu	Tyr	11e	Met	Ser
40		Thr	Leu	Pro 115	Glu	Leu	Ser	Asn	Thr 120	Lys	Leu	Tyr	Pro	Gly 125	Gln	Val	Trp
45		Thr	Ile 130	Ala	Asp	Leu	Leu	Gln 135	Ile	Thr	Val	Ser	<b>As</b> n 140	Ser	Ser	Asn	Ala
		Ala 145	Ala	Leu	Ile	Leu	Ala 150	Lys	Lys	Val	Ser	Lys 155	Asn	Thr	Ser	Asp	Phe 160
50		Val	Asp	Leu	Met	<b>As</b> n 165	Asn	Lys	Ala	Lys	Ala 170	Ile	Gly	Met	Lys	Asn 175	Thr
		His	Phe	Val	Asn 180	Pro	Thr	Gly	Ala	Glu 185	Asn	Ser	Arg	Leu	Arg 190	Thr	Phe
55		Ala	Pro	Thr 195	Lys	Tyr	Lys	qeA	Gln 200	Glu	Arg	Thr	Val	Thr 205	Thr	Ala	Arg

	Asp	Tyr 210	Ala	Ile	Leu	Asp	Leu 215	His	Val	Ile	Lys	Glu 220	Thr	Pro	Lys	Ile
5	Leu 225	Asp	Phe	Thr	Lys	Gln 230	Leu	Ala	Pro	Thr	Thr 235	His	Ala	Val	Thr	Tyr 240
	Tyr	Thr	Phe	Asn	Phe 245	Ser	Leu	Glu	Gly	Ala 250	Lys	Met	Ser	Leu	Pro 255	Gly
10	Thr	Asp	Gly	Leu 260	Lys	Thr	Gly	Ser	Ser 265	Asp	Thr	Ala	Asn	Tyr 270	Asn	His
	Thr	Ile	Thr 275	Thr	Lys	Arg	Gly	Lys 280	Phe	Arg	Ile	Asn	Gln 285	Val	Ile	Met
15	Gly	Ala 290	Gly	Asp	Tyr	Lys	Asn 295	Leu	Gly	Gly	Glu	<b>Lys</b>	Gln	Arg	Asn	Met
20	Met 305	Gly	Asn	Ala	Leu	<b>Met</b> 310	Glu	Arg	Ser	Phe	<b>As</b> p 315	Gln	Tyr	Lys	Tyr	<b>Val</b> 320
	Lys	Ile	Leu	Ser	<b>Lys</b> 325	Gly	Glu	Gln	Arg	Ile 330	Asn	Gly	Lys	Lys	Tyr 335	Tyr
25	Val	Glu	Asn	Asp 340	Leu	Tyr	Asp	Val	Leu 345	Pro	Ser	Asp	Phe	<b>Ser</b> 350	Lys	Lys
	Asp	Tyr	Lys 355	Leu	Val	Val	Glu	Asp 360	Gly	Lys	Val	His	Ala 365	Asp	Tyr	Pro
30	Arg	Glu 370	Phe	Ile	Asn	Lys	<b>As</b> p 375	Tyr	Gly	Pro	Pro	Thr 380	Val	Glu	Val	His
	Gln 385	Pro	Ile	Ile	Gln	Lys 390	Ala	Asn	Thr	Val	Ala 395	Lys	Ser	Met	Trp	Glu 400
35	Glu	His	Pro	Leu	Phe 405	Thr	Ile	Ile	Gly	Gly 410	Thr	Сув	Leu	Val	Ala 415	Gly
	Leu	Ala	Leu	Ile 420	Val	His	Met	Ile	Ile 425	Asn	Arg	Leu	Phe	Arg. 430	Lys	Arg
40	Lys															
(2)	INFO	RMAT:	ION 1	FOR S	SEQ :	ID N	D:52	33:								
45	(i)	(A) (B) (C)	UENCI ) LEI ) TYI ) STI ) TOI	NGTH PE: 8 RANDI	: 15: amino EDNES	1 am: 5 ac: 55:	ino a id sing	acid	S							
50	(ii)	MOL	ECUL	E TY	PE: ]	prot	ein									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

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5		Thr	Leu	Ala	Leu 20	Gly	Met	Ile	Ala	Thr 25	Thr	Gly	Ala	Thr	Val 30	Ala	Gly
		Asn	Glu	Val 35	Ser	Ala	Ala	Glu	Lys 40	Asp	Lys	Leu	Pro	Ala 45	Thr	Gln	Lys
10		Ala	Lys 50	Glu	Met	Gln	Asn	Val 55	Pro	Tyr	Thr	Ile	Ala 60	Val	Asp	Gly	Ile
		Met 65	Ala	Phe	Asn	Gln	Ser 70	Tyr	Leu	Asn	Leu	Pro 75	Lys	Asp	Ser	Gln	Leu 80
15		Ser	Tyr	Leu	Asp	Leu 85	Gly	Asn	Lys	Val	Lys 90	Ala	Leu	Leu	Tyr	Asp 95	Glu
20		Arg	Gly	Val	Thr 100	Pro	Glu	Lys	Ile	<b>Arg</b> 105	Asn	Ala	Lys	Ser	Ala 110	Val	Tyr
		Thr	Ile	Thr 115	Trp	Lys	Asp	Gly	Ser 120	Lys	Lys	Glu	Val	Asp 125	Leu	Lys	Lys
25		Asp	Ser 130	Tyr	Thr	Ala	Asn	Leu 135	Phe	Asp	Ser	Asn	Ser 140	Ile	Lys	Gln	Ile
		Asp 145	Ile	Asn	Val	Lys	Thr 150	Lys									
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35		(i)	(B)	LEN TYP	IGTH: PE: & RANDE	497 amino	ami aci	no a .d singl	cids	5							
		(ii)	MOLE	ECULE	E TYE	e: p	rote	in									
40																	
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<i>45</i>		Asn 1	His	Cys	Asn	Arg 5	Ile	Glu	Arg	Lys	Met 10	Ala	Met	Ser	Asn	Asn 15	Phe
		Lys	Asp	Asp	Ph <b>e</b> 20	Glu	Lys	Asn	Arg	Gln 25	Ser	Ile	Asp	Thr	Asn 30	Ser	His
50		Gln	Asp	His 35	Thr	Glu	Asp	Val	Glu 40	Lys	Asp	Gln	Ser	Glu 45	Leu	Glu	His
		Gln	Asp 50	Thr	Ile	Glu	Asn	Thr 55	Glu	Gln	Gln	Phe	Pro 60	Pro	Arg	Asn	Ala
55		Gln 65	Arg	Arg	Lys	Arg	Arg 70	Arg	Asp	Leu	Ala	Thr 75	Asn	His	Asn	Lys	Gln 80

	Val	His	Asn	Glu	ser 85	GIn	Thr	ser	GIU	90 90	ASN	vaı	GIII	ASII	95	Ala
5	Gly	Thr	Ile	<b>As</b> p	Asp	Arg	Gln	Val	Glu 105	Ser	Ser	His	Ser	Thr 110	Glu	Ser
	Gln	Glu	Pro 115	Ser	His	Gln	Asp	Ser 120	Thr	Pro	Gln	His	Glu 125	Glu	Glu	Tyr
10	Tyr	Asn 130	Lys	Asn	Ala	Phe	<b>Ala</b> 135	Met	Asp	Lys	Ser	His 140	Pro	Glu	Pro	Ile
	Glu 145	Asp	Asn	Asp	Lys	<b>His</b> 150	Asp	Thr	Ile	Lys	Asn 155	Ala	Glu	Asn	Asn	Thr 160
15	Glu	His	Ser	Thr	Val 165	Ser	Asp	Lys	Ser	Glu 170	Ala	Glu	Gln	Ser	Gln 175	Gln
20	Pro	Lys	Pro	Tyr 180	Phe	Thr	Thr	Gly	Ala 185	Asn	Gln	Ser	Glu	Thr 190	Ser	Lys
	Asn	Glu	His 195	Asp	Asn	Asp	Ser	Val 200	Lys	Gln	Asp	Gln	Asp 205	Glu	Pro	Lys
25	Glu	His 210	His	Asn	Gly	Lys	<b>Lys</b> 215	Ala	Ala	Ala	Ile	Gly 220	Ala	Gly	Thr	Ala
	Gly 225	Val	Ala	Gly	Ala	Ala 230	Gly	Ala	Met	Ala	Ala 235	Ser	Lys	Ala	Lys	Lys 240
30	His	Ser	Asn	Asp	Ala 245	Gln	Asn	Lys	Ser	<b>As</b> n 250	Ser	Gly	Lys	Ala	<b>As</b> n <b>25</b> 5	Asn
	Ser	Thr	Glu	<b>Asp</b> 260	Lys	Ala	Ser	Gln	Asp 265	Lys	Ser	Lys	Asp	His 270	His	Asn
35	Gly	Lys	Lys 275	Gly	Ala	Ala	Ile	Gly 280	Ala	Gly	Thr	Ala	Gly 285	Leu	Ala	Gly
	Gly	Ala 290	Ala	Ser	Lys	Ser	Ala 295		Ala	Ala	Ser	300 Lys	Pro	His	Ala	Ser
40	Asn 305	Asn	Ala	Ser	Gln	Asn 310	His	Asp	Glu	His	Asp 315	Asn	His	Asp	Arg	Asp 320
45	Lys	Glu	Arg	Lys	Lys 325	Gly	Gly	Met	Ala	330 Lys	Val	Leu	Leu	Pro	Leu 335	Ile
	Ala	Ala	Val	<b>Le</b> u 340		Ile	Gly	Ala	Leu 345	Ala	Ile	Phe	Gly	Gly 350		Ala
50	Leu	Asn	<b>Asn</b> 355		Asn	Asn	Gly	Thr 360		Glu	Asn	Lys	Ile 365		Asn	Thr
	Asn	Lys 370		Asn	Ala	Asp	Glu 375		Lys	Asp	Lys	<b>Asp</b>		Ser	Lys	Asp
55	Ala 385		Lys	Asp	Lys	Ser 390		Ser	Thr	Asp	Ser 395		Lys	Ser	Lys	Glu 400

		Asp	Gln	Asp	Lys	Ala 405	Thr	Lys	Asp	Glu	Ser 410	Asp	Asn	Asp	Gln	<b>As</b> n 415	Asn
5		Ala	Asn	Gln	Ala 420	Asn	Asn	Gln	Ala	Gln 425	Asn	Asn	Gln	Asn	Gln 430	Gln	Gln
		Ala	Asn	Gln 435	Asn	Gln	Gln	Gln	Gln 440	Gln	Gln	Arg	Gln	Gly 445	Gly	Gly	Gln
10		Arg	His 450	Thr	Val	Asn	Gly	Gln 455	Glu	Asn	Leu	Tyr	Arg 460	Ile	Ala	Ile	Gln
		Tyr 465	Tyr	Gly	Ser	Gly	Ser 470	Pro	Glu	Asn	Val	Glu 475	Lys	Ile	Arg	Arg	Ala 480
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30		(ii)	MOLI	ECULI	E TYI	PE: p	prote	ein									
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		Lys	His	His	Pro 20	Lys	Leu	Arg	Ser	Phe 25	Tyr	Ser	Ile	Arg	Lys 30	Ser	Thr
40		Leu	Gly	Val 35	Ala	Ser	Val	Ile	Val 40	Ser	Thr	Leu	Phe	Leu 45	Ile	Thr	Ser
45		Gln	His 50	Gln	Ala	Gln	Ala	Ala 55	Glu	Asn	Thr	Asn	Thr 60	Ser	Asp	Lys	Ile
		Ser 65	Glu	Asn	Gln	Asn	Asn 70	Asn	Ala	Thr	Thr	Thr 75	Gln	Pro	Pro	Lys	Asp 80
			»	Gln	Thr	Gln	Pro	Ala	Thr	Gln		Ala	Asn	Thr	Ala	Lys	Asn
50		Thr	ASII	<b>0111</b>		85					90					95	
50						85 <b>As</b> p	Glu	Ser	Leu	Lys 105		Ala	Ile	Lys	Asp 110	95	

	Gln	Leu 130	Leu	Asp	Lys	Asn	<b>Asn</b> 135	Glu	Thr	Gln	Tyr	Tyr 140	His	Phe	Phe	Ser
5	Ile 145	Lys	Asp	Pro	Ala	Asp 150	Val	Tyr	Tyr	Thr	Lys 155	Lys	Lys	Ala	Glu	Val 160
	Glu	Leu	Asp	Ile	Asn 165	Thr	Ala	Ser	Thr	Trp 170	Lys	Lys	Phe	Glu	Val 175	Tyr
10	Glu	Asn	Asn	Gln 180	Lys	Leu	Pro	Val	Arg 185	Leu	Val	Ser	Tyr	Ser 190	Pro	Val
	Pro	Glu	Asp 195	His	Ala	Tyr	Ile	<b>Arg</b> 200	Phe	Pro	Val	Ser	Asp 205	Gly	Thr	Gln
15	Glu	Leu 210	Lys	Ile	Val	Ser	Ser 215	Thr	Gln	Ile	Asp	Asp 220	Gly	Glu	Glu	Thr
	Asn 225	Tyr	Asp	Tyr	Thr	Lys 230	Leu	Val	Phe	Ala	Lys 235	Pro	Ile	Tyr	Asn	<b>Asp</b> 240
20	Pro	Ser	Leu	Val	Lys 245	Ser	Asp	Thr	Asn	<b>Asp</b> 250	Ala	Val	Val	Thr	Asn 255	Asp
25	Gln	Ser	Ser	Ser 260	Val	Ala	Ser	Asn	Gln 265	Thr	Asn	Thr	Asn	Thr 270	Ser	Asn
	Gln	Asn	Ile 275	Ser	Thr	Ile	Asn	Asn 280	Ala	Asn	Asn	Gln	Pro 285	Gln	Ala	Thr
30	Thr	Asn 290	Met	Ser	Gln	Pro	Ala 295	Gln	Pro	Lys	Ser	Ser 300	Thr	Asn	Ala	Asp
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35	Asn	Asp	Lys	Thr	Asn 325	Glu	Ser	Ser	Asn	Gln 330	Ser	Asp	Val	Asn	Gln 335	Gln
	Tyr	Pro	Pro	Ala 340	Asp	Glu	Ser		Gln 345		Ala	Ile		<b>Asn</b> 350		Ala
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40	Thr 385	Val	Glu	Pro	Ala	Thr 390	Val	Ile	Phe	Thr	<b>Lys</b> 395	Thr	Gly	Pro	Ile	Ile 400
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	Val	Lys 450	Ile	Val	Ser	Ser	Ile 455	Glu	Tyr	Gly	Glu	Asn 460	Ile	His	Glu	Asp
5	Tyr 465	Asp	Tyr	Thr	Leu	<b>Me</b> t 470	Val	Phe	Ala	Gln	Pro 475	Ile	Thr	Asn	Asn	Pro 480
	Asp	Asp	Tyr	Val	<b>Asp</b> 485	Glu	Glu	Thr	Tyr	Asn 490	Leu	Gln	Lys	Leu	Leu 495	Ala
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	Lys	Leu	Gln 515	Glu	Lys	Leu	Pro	Glu 520	Lys	Tyr	Lys	Ala	Glu 525	Tyr	Lys	Lys
15	Lys	<b>Le</b> u 530	Asp	Gln	Thr	Arg	Val 535	Glu	Leu	Ala	Asp	Gln 540	Val	Lys	Ser	Ala
20	Val 545	Thr	Glu	Phe	Glu	Asn 550	Val	Thr	Pro	Thr	Asn 555	Asp	Gln	Leu	Thr	Asp 560
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25	Ser	Val	Met	<b>Asp</b> 580	Gly	Phe	Val	Glu	His 585	Pro	Phe	Tyr	Thr	<b>Ala</b> 590	Thr	Leu
	Asn	Gly	Gln 595	Lys	Tyr	Val	Val	Met 600	Lys	Thr	Lys	Asp	<b>Asp</b> 605	Ser	Tyr	Trp
30	Lys	Asp 610	Leu	Ile	Val	Glu	Gly 615	Lys	Arg	Val	Thr	Thr 620	Val	Ser	Lys	Asp
	Pro 625	Lys	Asn	Asn	Ser	Arg 630	Thr	Leu	Ile	Phe	Pro 635	Tyr	Ile	Pro	Asp	Lys 640
35	Ala	Val	Tyr	Asn	Ala 645	Ile	Val	Lys	Val	<b>Val</b> 650	Val	Ala	Asn	Ile	Gly 655	Tyr
	Glu	Gly	Gln	Tyr 660	His	Val	Arg	Ile	Ile 665	Asn	Gln	Asp	Ile	<b>Asn</b> 670	Thr	Lys
40	Asp	Asp	<b>Asp</b> 675	Thr	Ser	Gln	Asn	Asn 680	Thr	Ser	Glu	Pro	Leu 685	Asn	Val	Gln
45	Thr	Gly 690	Gln	Glu	Gly	Lys	Val 695	Ala	Asp	Thr	Asp	Val 700	Ala	Glu	Asn	Ser
	Ser 705	Thr	Ala	Thr	Asn	Pro 710	Lys	Asp	Ala	Ser	<b>Asp</b> 715	Lys	Ala	Asp	Val	Ile 720
50	Glu	Pro	Glu	Ser	<b>Asp</b> 725	Val	Val	Lys	Asp	<b>Ala</b> 730	Asp	Asn	Asn	Ile	<b>Asp</b> 735	Lys
	Asp	Val	Gln	His 740	Asp	Val	Asp	His	Leu 745	Ser	Asp	Met	Ser	<b>Asp</b> 750	Asn	Asn
55	His	Phe	Asp 755	Lys	Tyr	Asp	Leu	<b>Lys</b> 760	Glu	Met	Asp	Thr	Gln 765	Ile	Ala	Lys

	Asp	770	Asp	Arg	Asn	Val	775	Lys	Asp	Ala	Asp	780	ser	Val	GIY	Met
5	<b>Ser</b> 785	Ser	Asn	Val	Asp	Thr 790	Asp	Lys	Asp	Ser	<b>As</b> n 795	Lys	Asn	Lys	Asp	Lys 800
	Val	Ile	Gln	Leu	<b>Asn</b> 805	His	Ile	Ala	Asp	Lys 810	Asn	Asn	His	Thr	Gly 815	Lys
10	Ala	Ala	Lys	Leu 820	Asp	Val	Val	Lys	Gln 825	Asn	Tyr	Asn	Asn	Thr 830	Asp	Lys
	Val	Thr	Asp 835	Lys	Lys	Thr	Thr	Glu 840	His	Leu	Pro	Ser	<b>Asp</b> 845	Ile	His	ГÀа
15	Thr	Val 850	Asp	Lys	Thr	Val	Lys 855	Thr	Lys	Glu	Lys	Ala 860	Gly	Thr	Pro	Ser
20	<b>Lys</b> 865	Glu	Asn	Lys	Leu	<b>Ser</b> 870	Gln	Ser	Lys	Met	<b>Le</b> u 875	Thr	Lys	Asn	Trp	<b>Arg</b> 880
	Asn	Asn	Xaa	Gln	Ala 885	Asn										
	(2) INFOR	TAMS	ON I	FOR S	SEQ :	D NO	523	36:								
25	(i)	(A) (B) (C)	LEN TYN	NGTH PE: 8 RANDI	: 236 amino EDNES	reris ami aci	ino a id singl	acids	3							
30	(ii)					linea										
35	(xi)	SEQ	JENC!	E DE:	SCRI	PTIOI	N: SI	EQ II	OM C	:523(	5:					
	Asn 1	Met	Asn	Lys	Asn 5	Val	Met	Val	Lys	Gly 10	Leu	Thr	Ala	Leu	Thr 15	Ile
40	Leu	Thr	Ser	Leu 20	Gly	Phe	Ala	Glu	Asn 25	Ile	Ser	Asn	Gln	Хаа 30	His	Ser
45	Ile	Ala	Lys 35	Ala	Glu	Lys	Asn	Val 40	Lys	Glu	Ile	Thr	Asp 45	Ala	Thr	Lys
	Glu	Pro 50	Tyr	Asn	Ser	Val	Val 55	Ala	Phe	Val	Gly	Gly 60	Thr	Gly	Val	Val
50	Val 65	Gly	Lys	Asn	Thr	Ile 70	Val	Thr	Asn	Lys	His 75	Ile	Ala	Lys	Ser	Asn 80
	Asp	Ile	Phe	Lys	Asn 85	Arg	Val	Ser	Ala	His 90	His	Ser	Ser	Lys	Gly 95	Lys
55	Gly	Gly	Gly	Asn 100		qaA	Val	Lys	<b>Asp</b> 105	Ile	Val	Glu	Tyr	Pro 110	Gly	Lys

	Glu	Asp	Leu 115	Ala	Ile	Val	His	Val 120	His	Glu	Thr	Ser	Thr 125	Glu	Gly	Leu
5	Asn	Phe 130	Asn	Lys	Asn	Val	Ser 135	Tyr	Thr	Lys	Phe	Ala 140	Ąsp	Gly	Ala	Lys
	Val 145	Lys	Asp	Arg	Ile	<b>Ser</b> 150	Val	Ile	Gly	Tyr	Pro 155	Lys	Gly	Ala	Gln	Thr 160
10	Lys	Tyr	Lys	Met	Phe 165	Glu	Ser	Thr	Gly	Thr 170	Ile	Asn	His	Ile	Ser 175	Gly
	Thr	Phe	Met	Glu 180	Phe	Asp	Ala	Tyr	Ala 185	Gln	Pro	Gly	Asn	Ser 190	Gly	Ser
15	Pro	Val	Leu 195	Asn	Ser	Lys	His	<b>Xaa</b> 200	Leu	Ile	Gly	Ile	<b>Le</b> u 205	Tyr	Ala	Gly
20	Ser	Gly 210	Lys	Asp	Glu	Ser	Glu 215	Lys	Asn	Phe	Gly	Val 220	Tyr	Phe	Thr	Pro
20	Gln 225	Leu	Xaa	Xaa	Phe	Ile 230	Pro	Asn	Asn	Ile	Glu 235	Lys				
(2)	INFO	TAMS	ON E	FOR S	SEQ 1	D NO	523	37:								
25	(i)	(A) (B)	LEN TYP	NGTH:	ARACT : 363 amino EDNES	ami aci	.no a .d	cids	3							
30	(ii)				3Y: 1 PE: p											
35	(xi)	SEQU	JENCE	E DES	SCRIF	MOIT	I: SE	Q II	NO:	5237	' :					
	Tyr 1	Arg	Leu	Glu	His 5	Thr	Ile	Met	Lys	Met 10	Arg	Thr	Ile	Ala	Lys 15	Thr
40	Ser	Leu	Ala	Leu 20	Gly	Leu	Leu	Thr	Thr 25	Gly	Ala	Ile	Thr	Val 30	Thr	Thr
45	Gln	Ser	Val 35	Lys	Ala	Glu	Lys	Ile 40	Gln	Ser	Thr	Lys	<b>Val</b> <b>4</b> 5	Asp	Lys	Val
	Pro	Thr 50	Leu	Lys	Ala	Glu	Arg 55	Leu	Ala	Met	Ile	Asn 60	Ile	Thr	Ala	Gly
50	Ala 65	Asn	Ser	Ala	Thr	Thr 70	Gln	Ala	Ala	Asn	Thr 75	Arg	Gln	Glu	Arg	Thr 80
	Pro	Lys	Leu	Glu	Lys 85	Ala	Pro	Asn	Thr	Asn 90	Glu	Glu	Lys	Thr	<b>Se</b> r 95	Ala
<i>55</i>	Ser	Lys	Tle	Glu	Lve	Tle	Sar	C1 n	Dwa	T	<b>~1</b> ~	<u>ما</u>	-1		_	Th-

		ьец	nea	11e 115	ser	Ala	Thr	Pro	120	PIO	rys	GIN	GIU	125	Ser	GIII	Inr
5		Thr	Thr 130	Glu	Ser	Thr	Thr	Pro 135	Lys	Thr	Lys	Val	Thr 140	Thr	Pro	Pro	Ser
		Thr 145	Asn	Thr	Pro	Gln	Pro 150	Met	Gln	Ser	Thr	Lys 155	Ser	Asp	Thr	Pro	Gln 160
10		Ser	Pro	Thr	Ile	Lys 165	Gln	Ala	Gln	Thr	<b>As</b> p 170	Met	Thr	Pro	Lys	Tyr 175	Glu
15		Asp	Leu	Arg	Ala 180	Tyr	Tyr	Thr	ГÀЗ	Pro 185	Ser	Phe	Glu	Phe	Glu 190	Lys	Gln
		Phe	Gly	Phe 195	Met	Leu	Lys	Pro	Trp 200	Thr	Thr	Val	Arg	Phe 205	Met	Asn	Val
20		Ile	Pro 210	Asn	Arg	Phe	Ile	Tyr 215	Lys	Ile	Ala	Leu	Val 220	Gly	Lys	Asp	Glu
		Lys 225	Lys	Tyr	Lys	Asp	Gly 230	Pro	Tyr	Asp	Asn	Ile 235	Asp	Val	Phe	Ile	Val 240
25		Leu	Glu	Asp	Asn	Lys 245	Tyr	Gln	Leu	Lys	Lys 250	Tyr	Ser	Val	Gly	Gly 255	Ile
		Thr	Lys	Thr	Asn 260	Ser	Lys	Lys	Val	Asn 265	His	Lys	Val	Glu	Leu 270	Ser	Ile
30		Thr	Lys	Lys 275	Asp	Asn	Gln	Gly	Met 280	Ile	Ser	Arg	Asp	Val 285	Ser	Glu	Tyr
35		Met	Ile 290	Thr	Lys	Glu	Glu	Ile 295	Ser	Leu	Lys	Glu	Leu 300	Asp	Phe	Lys	Leu
		Arg 305	Lys	Gln	Leu	Ile	Glu 310	Lys	His	Asn	Leu	Tyr 315	Gly	Asn	Met	Gly	Ser 320
40		Gly	Thr	Ile	Val	Ile 325	Lys	Met	Lys	Asn	Gly 330	Gly	Lys	Tyr	Thr	Phe 335	Glu
		Leu	His	Lys	Lys 340	Leu	Gln	Glu	His	Arg 345	Met	Ala	Asp	Val	Ile 350	Asp	Gly
45		Thr	Asn	Ile 355	Asp	Asn	Ile	Glu	Val 360	Asn	Ile	Lys					
	(2) I	NFOF	TAMS	ON I	FOR S	SEQ :	ID NO	52:	38:								
50		(i)	(A) (B) (C)	LEI TYI	NGTH PE: & RANDI	ARAC: 150 amino EDNES	0 am: o ac: SS: s	ino a id sing:	acids	5							
55	_																

(ii) MOLECULE TYPE: protein

	(xi)	SEQU	JENC	E DES	SCRIE	PTION	1: SI	EQ II	ONO:	5238	3:					
5	Phe 1	Met	Lys	Phe	Lys 5	Ser	Leu	Ile	Thr	Thr 10	Thr	Leu	Ala	Leu	Gly 15	Val
	Leu	Ala	Ser	Thr 20	Gly	Ala	Asn	Phe	Asn 25	Asn	Asn	Glu	Ala	Ser 30	Ala	Ala
10	Ala	Lys	Pro 35	Leu	Asp	Lys	Ser	Ser 40	Ser	Ser	Leu	His	His 45	Gly	Tyr	Ser
	Lys	Val 50	His	Val	Pro	Tyr	Ala 55	Ile	Thr	Val	Asn	Gly 60	Thr	Ser	Gln	Asn
15	Ile 65	Leu	Ser	Ser	Leu	Thr 70	Phe	Asn	Lys	Asn	Gln 75	Asn	Ile	Ser	Tyr	Lys 80
20	Asp	Leu	Glu	Asp	Arg 85	Val	Lys	Ser	Val	Leu 90	Lys	Ser	Asp	Arg	Gly 95	Ile
20	Ser	Asp	Ile	Asp 100	Leu	Arg	Leu	Ser	Lys 105	Gln	Ala	Lys	Tyr	Thr 110	Val	Tyr
25	Phe	Lys	Asn 115	Gly	Thr	Lys	Lys	Val 120	Ile	Asp	Leu	Lys	Ala 125	Gly	Ile	Tyr
	Thr	Ala 130	Asp	Leu	Ile	Asn	Thr 135	Ser	Glu	Ile	Lys	Ala 140	Ile	Asn	Ile	Asn
30	Val 145	Asp	Thr	Lys	Lys	Gln 150										
	(2) INFOR	TAM!	ON I	FOR S	SEQ I	D NO	523	39:								
35	(i)	(A) (B) (C)	LEN TYI STI	NGTH: PE: 8 RANDI	239 amino EDNES	TERIS  ami  aci  SS: s  lines	ino a id singl	cids	5							
40	(ii)	MOLE	CULI	E TYI	PE: p	prote	ein									
45	(xi)	SEQU	JENCI	E DES	SCRII	PTION	N: SI	EQ II	ои о	: 523	€:					
	Glu 1	Lys	Arg	Phe	Met 5	Gln	Met	Ala	Arg	Lys 10	Val	Val	Val	Val	Asp 15	Asp
50	Glu	Lys	Pro	Ile 20	Ala	Asp	Ile	Leu	Glu 25	Phe	Asn	Leu	Lys	Lys 30	Glu	Gly
	Tyr	Asp	Val 35	Tyr	Cys	Ala	Tyr	Asp 40	Gly	Asn	Asp	Ala	Val 45	Asp	Leu	Ile
55	Tyr	Glu 50	Glu	Glu	Pro	Asp	Ile 55	Val	Leu	Leu	Asp	Ile 60	Met	Leu	Pro	Gly

		Arg 65	Asp	Gly	Met	Glu	Val 70	Сув	Arg	Glu	Val	Arg 75	Lys	Lys	Tyr	Glu	Met 80
5		Pro	Ile	Ile	Met	Leu 85	Thr	Ala	Lys	Asp	Ser 90	Glu	Ile	Asp	Lys	Val 95	Leu
		Gly	Leu	Glu	Leu 100	Gly	Ala	qeA	qeA	Tyr 105	Val	Thr	ГÀЗ	Pro	Phe 110	Ser	Thr
10		Arg	Glu	Leu 115	Ile	Ala	Arg	Val	Lys 120	Ala	Asn	Leu	Arg	Arg 125	His	Tyr	Ser
		Gln	Pro 130	Ala	Gln	Asp	Thr	Gly 135	Asn	Val	Thr	Asn	Glu 140	Ile	Thr	Ile	Lys
15		Asp 145	Ile	Val	Ile	Tyr	Pro 150	Asp	Ala	Tyr	Ser	Ile 155	Lys	Lys	Arg	Gly	Glu 160
20		Asp	Ile	Glu	Leu	Thr 165	His	Arg	Glu	Phe	<b>Glu</b> 170	Leu	Phe	His	Tyr	Leu 175	Ser
20		Lys	His	Met	Gly 180	Gln	Val	Met	Thr	Arg 185	Glu	His	Leu	Leu	Gln 190	Thr	Val
25		Trp	Gly	Tyr 195	Asp	Tyr	Phe	Gly	Asp 200	Val	Arg	Thr	Val	Asp 205	Val	Thr	Ile
		Arg	Arg 210	Leu	Arg	Glu	Lys	Ile 215	Glu	Asp	Asp	Pro	Ser 220	His	Pro	Glu	Tyr
30		Ile 225	Val	Thr	Arg	Arg	Gly 230	Val	Gly	Tyr	Phe	<b>Leu</b> 235	Gln	Gln	His	Glu	
	(2)	INFO	TAMS	ION I	FOR S	SEQ :	ID NO	0:524	10:								
35		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 6 RANDI	ARACT : 13: amino EDNES GY:	3 am: 5 ac: 5S: 5	ino a id singl	acids	3							
40		(ii)	MOLI	ECULI	E TY	PE: I	prote	ein									
		(xi)	SEQ	JENC	E DES	SCRI	PTIO	N: SI	EQ II	ON C	: 524	0:					
45		Xaa 1	Leu	Ser	Thr	Val 5	Ile	Gly	Ala	Xaa	Leu 10	Phe	Phe	Lys	Ser	Ser 15	Val
50		Ser	Leu	Val	Phe 20	Lys	Met	Val	Lys	<b>Lys</b> 25	Phe	Arg	Xaa	Gly	Val 30	Ile	Ser
		Val	Asn	Asp 35	Val	Met	Phe	Ser	Ser 40	Ser	Ile	Met	Tyr	Arg 45	Ile	Lys	Lys
55		Asn	Ala 50	Phe	Ser	Leu	Thr	Val 55	Met	Ala	Ile	Ile	Ser 60	Ala	Ile	Thr	Val

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys 85			Ser 65	Val	Leu	Суз	Phe	Ala 70	Ala	Ile	Ser	Arg	Ala 75	Ser	Leu	Ser	Ser	Glu 80
TYT ASN TYT LYS Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu 115  Phe Asp Val Lys Ala 130  15  (2) INFORMATION FOR SEQ ID NO:5241:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 508 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1 5 15  Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly 20 25  Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro 40  Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp 50  Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser 70  Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ash Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	5		Ile	Lys	Tyr	Thr		Pro	His	qsA	Val		Ile	Lys	Asp	Gln		Lys
Phe Asp Val Lys Ala			Ala	Asn	Gln		Ala	Ser	Glu	Leu		Asn	Gln	Lys	Ile		His	Phe
(2) INFORMATION FOR SEQ ID NO:5241:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 508 amino acids (B) TYPE: amino acids (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein  (ii) MOLECULE TYPE: protein  (iii) MOLECULE TYPE: protein  (iii) MOLECULE TYPE: protein  (iv) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1	10		Tyr	Asn		Lys	Glu	Val	Ile		Thr	Lys	Leu	Tyr		Asp	Asn	Leu
(2) INFORMATION FOR SEQ ID NO:5241:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 508 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1 5 10 15  Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly 20 25  Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro 35 40 45  Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp 50 55  Leu Thr Ser Lys Ser Glu Arg Ala Gln Glu Ala Phe Glu Ser Trp Ser 65 70 75 80  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115 Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 116 Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu			Phe		Val	Lys	Ala											
(A) LENGTH: 508 amino acids (B) TYPE: amino acids (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein  (iii) MOLECULE TYPE: protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  (xi) MOLECULE TYPE: protein  25  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  (xi) MOLECULE TYPE: protein  26  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  (xi) MOLECULE TYPE: protein  26  (xi) MOLECULE TYPE: protein  26  (xi) MOLECULE TYPE: protein  27  (xi) MOLECULE TYPE: protein  28  (xi) MOLECULE TYPE: protein  29  (xi) MOLECULE TYPE: protein  25  (xi) MOLECULE TYPE: protein  26  (xi) MOLECULE TYPE: protein  27  (xi) MOLECULE TYPE: protein  26  (xi) MOLECULE TYPE: protein  27  (xi) MOLECULE TYPE: protein  28  (xi) MOLECULE TYPE: protein  29  (xi) MOLE	15	(2)	INFOR	RMAT:	ON I	FOR S	SEQ 1	ID NO	524	11:								
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1	20		(i)	(A) (B) (C)	LEN TYI STI	NGTH: PE: 8 RANDI	: 508 amino EDNES	Bami baci SS: 8	ino a id singl	acids	3							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:  Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1			(ii)	MOL	ECULE	E TY	PE: p	prote	ein									
Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val 1 10	25																	
Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly 25  Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro 45  Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp 50  Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser 70  Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 135  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu			(xi)	SEQU	JENCE	E DES	SCRIE	PTION	1: SI	EQ II	NO:	5241	L:					
Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro 35  Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp 55  Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser 65  Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	30			Ile	Tyr	Ile		Ala	Asn	Lys	Gln		Arg	Asp	Asn	Met		Val
Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp 50  Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser 70  Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu			Asn	Val	Arg		Tyr	Ile	Ala	Glu		Tyr	Gly	Leu	Phe		Asn	Gly
Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser 70  Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 135  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	35		Glu	Phe		Lys	Gly	Ser	Ser		Glu	Thr	Ile	Glu		Thr	Asn	Pro
Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp 85  Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100  Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu			Ala		Gly	Glu	Thr	Leu		His	Ile	Thr	Arg		Lys	Asp.	Lys	Asp
Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn 100 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115 Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	40			Asp	His	Ala	Val	-	Val	Ala	Gln	Glu		Phe	Glu	Ser	Trp	
Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala 115  Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	45		Leu	Thr	Ser	Lys		Glu	Arg	Ala	Gln		Leu	Arg	Asp	Ile		Asp
Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly 130 135 140  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu			Lys	Leu	Met		Gln	Lys	Asp	Lys		Ala	Met	Ile	Glu		Leu	Asn
130 135 140  Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu	50		Asn	Gly		Pro	Ile	Arg	Glu		Thr	Ala	Ile	Asp		Pro	Phe	Ala
			Ala	-	His	Phe	His	Tyr		Ala	Ser	Val	Ile		Thr	Glu	Glu	Gly
	55			Val	Asn	Asp	Ile		Lys	Asp	Thr	Met		Ile	Val	Arg	His	Glu 160

	Pro	Ile	Gly	Val	<b>Val</b> 165	Gly	Ala	Val	Val	<b>Ala</b> 170	Trp	Asn	Phe	Pro	<b>Met</b> 175	Leu
5	Leu	Ala	Ala	Trp 180	Lys	Ile	Ala	Pro	Ala 185	Ile	Ala	Ala	Gly	<b>Asn</b> 190	Thr	Ile
	Val	Ile	Gln 195	Pro	Ser	Ser	Ser	Thr 200	Pro	Leu	Ser	Leu	Leu 205	Glu	Val	Ala
10	Lys	Ile 210	Phe	Gln	Glu	Val	<b>Le</b> u 215	Pro	Lys	Gly	Val	Val 220	Asn	Ile	Leu	Thr
	Gly 225	Lys	Gly	Ser	Glu	Ser 230	Gly	Asn	Ala	Ile	Phe 235	Asn	His	Asp	Gly	Val 240
15	Asp	Lys	Leu	Ser	Phe 245	Thr	Gly	Ser	Thr	<b>As</b> p 250	Val	Gly	Tyr	Gln	Val 255	Ala
20	Glu	Ala	Ala	Ala 260	Lys	His	Leu	Val	Pro 265	Ala	Thr	Leu	Glu	Leu 270	Gly	Gly
20	Lys	Ser	Ala 275	Asn	Ile	Ile	Leu	Asp 280	Asp	Ala	Asn	Leu	Asp 285	Leu	Ala	Val
25	Glu	Gly 290	Ile	Gln	Leu	Gly	Ile 295	Leu	Phe	Asn	Gln	Gly 300	Glu	Val	Cys	Ser
	Ala 305	Gly	Ser	Arg	Leu	Leu 310	Val	His	Glu	Lys	Ile 315	Tyr	Asp	Gln	Leu	Val 320
30	Pro	Arg	Leu	Gln	Glu 325	Ala	Phe	Ser	Asn	Ile 330	Lys	Val	Gly	Asn	Pro 335	Gln
	Asp	Glu	Ala	Thr 340	Gln	Met	Gly	Ser	Gln 345	Thr	Gly	Lys	Asp	Gln 350	Leu	Asp
35	Lys	Ile	Gln 355	Ser	Tyr	Ile	Asp	<b>Ala</b> 360	Ala	Lys	Glu	Ser	<b>Asp</b> 365	Ala	Gln	Ile
	Leu	Ala 370	Gly	Gly	His	Arg	Leu 375	Thr	Glu	Asn	Gly	Leu 380	Asp	Lys	Gly	Phe
40	Phe 385	Phe	Glu	Pro	Thr	<b>Le</b> u 390	Ile	Ala	Val	Pro	<b>As</b> p 395	Asn	His	His	Lys	Leu 400
	Ala	Gln	Glu	Glu	Ile 405	Phe	Gly	Pro	Val	Leu 410	Thr	Val	Ile	Lys	Val 415	Lys
45	Asp	Asp	Gln	Glu 420	Ala	Ile	Asp	Ile	Ala 425	Asn	Asp	Ser	Glu	Tyr 430	Gly	Leu
50	Ala	Gly	Gly 435	Val	Phe	Ser	Gln	Asn 440	Ile	Thr	Arg	Ala	Leu 445	Asn	Ile	Ala
	Lys	Ala 450	Val	Arg	Thr	Gly	Arg 455	Ile	Trp	Ile	Asn	Thr 460	Tyr	Asn	Gln	Val
	Pro 465	Glu	Gly	Ala	Pro	Phe 470	Gly	Gly	Tyr	Lys	Lys 475	Ser	Gly	Ile	Gly	Arg 480

		Glu	Thr	Tyr	Lys	Gly 485	Ala	Leu	Ser	Asn	Tyr 490	Gln	Gln	Val	Lys	Asn 495	Ile
5		Tyr	Ile	Asp	Thr 500	Ser	Asn	Ala	Leu	<b>Lys</b> 505	Gly	Leu	Tyr				
	(2)	INFO	RMAT	ION	FOR	SEQ	ID N	0:52	42:								
10		(i)	(A (B (C	) LE: ) TY: ) ST:	NGTH PE: RAND	ARAC : 54 amin EDNE GY:	0 am. o ac: SS: :	ino id sing	acid	s							
15		(ii)	MOL	ECUL:	E TY	PE: ]	prote	ein									
		(xi)	SEQ	UENC	E DE:	SCRI	PTIO	N: S	EQ II	ono	: 524:	2:					
20		Asn 1	His	Leu	Thr	Ala 5	Arg	Ile	Ile	Asn	Gln 10	Glu	Asp	Asp	Leu	Met 15	Ası
25		Leu	Phe	Arg	Gln 20	Gln	Lys	Phe	Ser	Ile 25	Arg	Lys	Phe	Asn	Val 30	Gly	Ile
		Phe	Ser	Ala 35	Leu	Ile	Ala	Thr	Val 40	Thr	Phe	Ile	Ser	Thr 45	Asn	Pro	Thi
30		Thr	Ala 50	Ser	Ala	Ala	Glu	Gln 55	Asn	Gln	Pro	Ala	Gln 60	Asn	Gln	Pro	Ala
		Gln 65	Pro	Ala	Asp	Ala	Asn 70	Thr	Gln	Pro	Asn	Ala 75	Asn	Ala	Gly	Ala	Glr 80
35		Ala	Asn	Pro	Thr	Ala 85	Gln	Pro	Ala	Ala	Pro 90	Ala	Asn	Gln	Gly	Gln 95	Pro
		Ala	Val	Gln	Pro 100	Ala	Asn	Gln	Gly	Gly 105	Gln	Ala	Asn	Pro	Ala 110	Gly	Gly
40		Ala	Ala	Gln 115	Pro	Asn	Thr	Gln	Pro 120	Ala	Gly	Gln	Gly	Asp 125	Gln	Ala	Asp
		Pro	Asn 130	Asn	Ala	Ala	Gln	Ala 135	Gln	Pro	Gly	Asn	Gln 140	Ala	Thr	Pro	Ala
45		Asn 145	Gln	Ala	Gly	Gln	Gly 150	Asn	Asn	Gln	Ala	Thr 155	Pro	Asn	Asn	Asn	Ala 160
50		Thr	Pro	Ala	Asn	Gln 165	Thr	Gln	Pro	Ala	Asn 170	Ala	Pro	Ala	Ala	Ala 175	Glr
		Pro	Ala	Ala	Pro 180	Val	Ala	Ala	Asn	Ala 185	Gln	Thr	Gln	Asp	Pro 190	Asn	Ala

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp 195 200 205

	Pro	Ala 210	Ile	Ser	Thr	Asp	G1u 215	Asn	Arg	GIn	Asp	220	Tnr	Val	inr	vai
5	Thr 225	Asp	Lys	Val	Asn	Gly 230	Tyr	Ser	Leu	Ile	<b>As</b> n 235	Asn	Gly	Lys	Ile	Gly 2 <b>4</b> 0
	Phe	Val	Asn	Ser	Glu 245	Leu	Arg	Arg	Ser	<b>Asp</b> 250	Met	Phe	Asp	Lys	Asn 255	Asn
10	Pro	Gln	Asn	Tyr 260	Gln	Ala	Lys	Gly	<b>A</b> sn 265	Val	Ala	Ala	Leu	Gly 270	Arg	Val
	Asn	Ala	Asn 275	Asp	Ser	Thr	Asp	His 280	Gly	Asn	Phe	Asn	Gly 285	Ile	Ser	Lys
15	Thr	Val 290	Asn	Val	Lys	Pro	Asp 295	Ser	Glu	Leu	Ile	Ile 300	Asn	Phe	Thr	Thr
20	Met 305	Gln	Thr	Asn	Ser	Lys 310	Gln	Gly	Ala	Thr	Asn 315	Leu	Val	Ile	Lys	Asp 320
20	Ala	Lys	Lys	Asn	Thr 325	Glu	Leu	Ala	Thr	<b>Val</b> 330	Asn	Val	Ala	Lys	Thr 335	Gly
25	Thr	Ala	His	Leu 340	Phe	Lys	Val	Pro	Thr 345	Asp	Ala	Asp	Arg	Leu 350	Asp	Leu
	Gln	Phe	Ile 355	Pro	Asp	Asn	Thr	Ala 360	Val	Ala	Asp	Ala	<b>Ser</b> 365	Arg	Ile	Thr
30	Thr	<b>As</b> n 370	Lys	Asp	Gly	Tyr	<b>Lys</b> 375	Tyr	Tyr	Ser	Phe	Ile 380	Yab	Asn	Val	Gly
	Leu 385	Phe	Ser	Gly	Ser	His 390	Leu	Tyr	Val	Lys	<b>As</b> n 395	Arg	Asp	Leu	Ala	Pro 400
35	Lys	Ala	Thr	Asn	Asn 405	Lys	Glu	Tyr	Thr	Ile 410	Asn	Thr	Glu	Ile	Gly 415	Asn
		-		420					425					430		Glu
40	Val	Thr	Leu 435	Pro	Gln	Gly	Val	Thr 440	Tyr	Val	Asn	Asn	Ser 445	Leu	Thr	Thr
	Thr	Phe 450	Pro	Asn	Gly	Asn	Glu 455	Asp	Ser	Thr	Val	Leu 460		Asn	Met	Thr
45	Val 465		Tyr	Asp	Gln	<b>Asn</b> 470		Asn	Lys	Val	Thr 475		Thr	Ser	Gln	Gly 480
50	Val	Thr	Thr	Ala	Arg 485	Gly	Thr	His	Thr	Lys 490		Val	Leu	Phe	Pro 495	Asp
	Lys	Ser	Leu	Lys 500		Ser	Tyr	Lys	<b>Val</b> 505		Val	Ala	Asn	1le 510		Thr
55	Pro	Lys	<b>A</b> sn 515		Asp	Phe	Asn	Glu 520		Leu	Thr	Tyr	Arg 525		Ala	Ser

		Asp	<b>Val</b> 530	Val	Ile	Asn	Asn	Ala 535	Gln	Pro	Glu	Val	His 540				
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10		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 8 RANDI	ARACT : 274 amino EDNES GY: 1	1 am: 5 ac: 55: 1	ino a id sing:	acids	3							
		(ii)	MOLI	ECULI	E TYI	PE: p	prote	ein									
15		(xi)	SEQU	JENCI	E DES	SCRII	PTIO	1: S1	EQ II	NO:	: 5243	3 :					
20		Ile 1	Thr	Leu	Lys	Thr 5	Val	Ser	Gln	Leu	Ile 10	Asp	Met	Lys	Gln	Lys 15	Gln
20		Thr	Lys	Ile	Ser 20	Met	Val	Thr	Ala	Tyr 25	Asp	Phe	Pro	Ser	Ala 30	Lys	Gln
25		Val	Glu	Ala 35	Ala	Gly	Ile	Asp	Met 40	Ile	Leu	Val	Gly	Asp 45	Ser	Leu	Gly
		Met	Thr 50	Val	Leu	Gly	Tyr	Glu 55	Ser	Thr	Val	Gln	Val 60	Thr	Leu	Ala	Asp
30		Met 65	Ile	His	His	Gly	Arg 70	Ala	Val	Arg	Arg	Gly 75	Ala	Pro	Asn	Thr	Phe 80
		Val	Val	Val	Asp	Met 85	Pro	Ile	Gly	Ala	Val 90	Gly	Ile	Ser	Met	Thr 95	Gln
35		Asp	Leu	Asn	His 100	Ala	Leu	Lys	Leu	Tyr 105	Gln	Glu	Thr	Asn	Ala 110	Asn	Ala
		Ile	Lys	Ala 115	Glu	Gly	Ala	His	Ile 120	Thr	Pro	Phe	Ile	Glu 125	Lys.	Ala	Thr
40			130					135					140				Ser
45		145				Gly	150					155					160
		Glu	Gln	Leu	Ile	Leu 165	Asp	Ala	Lys	Asn	Val 170	Glu	Gln	Ala	Gly	Ala 175	Val
50					180	Glu				185					190		
				195		Ile			200					205			
55		Asp	Gly 210	Gln	Val	Leu	Val	Tyr 215	His	Asp	Met	Leu	Asn 220	Tyr	Gly	Val	Glu

		His 225	Lys	Ala	Lys	Phe	Val 230	Lys	Gln	Phe	Ala	<b>Asp</b> 235	Phe	Ser	Val	Gly	Val 240
5		Asp	Gly	Leu	Lys	Gln 245	Tyr	qaA	Gln	Glu	Val 250	Lys	Ser	Gly	Ala	Phe 255	Pro
		Ser	Glu	Glu	Tyr 260	Thr	Tyr	Lys	ГÀЗ	Lys 265	Ile	Met	Asn	Glu	<b>Val</b> 270	Asn	Asn
10		Asn	Asp														
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15		(i)	(A) (B) (C)	LEI TYI STI	NGTH:	430 amino EDNES	am: ac: SS: 8	sing]	acida	3							
20		(ii)	MOLE	ECULI	E TYI	PE: I	rote	ein									
25		(xi)	SEQU	JENCI	E DES	SCRI	PTIO	1: SI	EQ II	ON C	524	<b>1</b> :					
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30		Arg	Met	Lys	His 20	Gln	Glu	Thr	Thr	Ser 25	Gln	Gln	Tyr	Asn	Phe 30	Ser	Ile
		Ile	Lys	His 35	Gly	Asp	Ile	Ser	Thr 40	Pro	Gln	Gly	Phe	Thr 45	Ala	Gly	Gly
35		Met	His 50	Ile	Gly	Leu	Arg	Ala 55	Asn	Lys	Lys	Asp	Phe 60	Gly	Trp	Ile	Tyr
		Ser 65	Ser	Ser	Leu	Ala	Ser 70	Ala	Ala	Ala	Val	Tyr 75	Thr	Leu	Asn	Gln	Phe 80
40		Lys	Ala	Ala	Pro	Leu 85	Ile	Val	Thr	Glu	Asp 90	Thr	Leu	Gln	Lys	Ser 95	Lys
		Gly	Lys	Leu	Gln 100	Ala	Leu	Val	Val	Asn 105	Ser	Ala	Asn	Ala	<b>A</b> sn 110	Ser	Cys
45		Thr	Gly	Gln 115	Gln	Gly	Ile	Asp	<b>Asp</b> 120	Ala	Arg	Gln	Thr	Gln 125	Thr	Trp	Val
50		Ala	Gln 130	Gln	Leu	Gln	Ile	Pro 135	Ser	Glu	His	Val	Ala 140	Val	Ala	Ser	Thr
50		Gly 145	Val	Ile	Gly	Glu	Tyr 150	Leu	Pro	Met	Asp	Lys 155	Ile	Lys	Thr	Gly	Thr 160
c c		Glu	His	Ile	Lys	Asp 165	Ala	Asn	Phe	Ala	Thr 170	Pro	Gly	Ala	Phe	Asn 175	Glu
55																	

	Ala	a Ile	Leu	Thr 180	Thr	Asp	Thr	Cys	Thr 185	Lys	His	Ile	Ala	<b>Val</b> 190	Ser	Leu
5	Lys	3 Ile	<b>A</b> sp 195		Lys	Thr	Val	Thr 200	Ile	Gly	Gly	Ser	Thr 205	Lys	Gly	Ser
	Gly	/ Met 210	Ile	His	Pro	<b>As</b> n	Met 215	Ala	Thr	Met	Leu	Ala 220	Phe	Ile	Thr	Thr
10	Asr 225	Ala	Ser	Ile	Glu	Ser 230	Asn	Thr	Leu	His	Gln 235	Leu	Leu	Lys	Ser	Ser 240
15	Thr	Asp	His	Thr	Phe 245	Asn	Met	Ile	Thr	Val 250	Asp	Gly	Asp	Thr	<b>Ser</b> 255	Thr
75	Asr	Asp	Met	Val 260	Leu	Val	Met	Ala	Asn 265	His	Gln	Val	Glu	His 270	Gln	Ile
20	Leu	ser	Gln 275	Asp	His	Pro	Gln	Trp 280	Glu	Thr	Phe	Val	Asp 285	Ala	Phe	Asn
	Phe	Val 290	Cys	Thr	Phe	Leu	Ala 295	Lys	Ala	Ile	Ala	Arg 300	Asp	Gly	Glu	Gly
25	Ala 305	Thr	Lys	Leu	Ile	<b>Ser</b> 310	Val	Asn	Val	Ser	Gly 315	Ala	Lys	Ser	Ile	Ser 320
	Asp	Ala	Arg	Lys	Ile 325	Gly	Lys	Thr	Ile	Val 330	Ser	Ser	Asn	Leu	Val 335	Lys
30	Ser	Ala	Ile	Phe 340	Gly	Glu	Asp	Ala	Asn 345	Phe	Gly	Arg	Ile	Ile 350	Thr	Ala
35	Ile	Gly	Tyr 355	Ser	Gly	Cys	Glu	Ile 360	Asp	Pro	Asn	Cys	Thr 365	Tyr	Val	Gln
	Leu	Asn 370	Gln	Ile	Pro	Val	Val 375	Asp	Lys	Gly	Met	Ala 380	Val	Leu	Phe	Asp
40	Glu 385	Gln	Ala	Met	Ser	Asn 390	Thr	Leu	Thr	His	Glu 395		Val	Thr	Ile	Asp 400
	Val	Gln	Leu	Gly	Leu 405	Gly	Asn	Ala	Ala	Ala 410	Thr	Ala	Tyr	Gly	Cys 415	Asp
45	Leu	Ser	Tyr	<b>Asp</b> 420	Tyr	Val	Arg	Ile	Asn 425	Ala	Ser	Tyr	Arg	Thr 430		
	(2) INFO	RMAT:	ION I	FOR S	SEQ 1	D NO	0:524	15:								
50	(i)	(B)	JENCE LEN TYI	NGTH: PE: & RANDE	469 Amino EDNES	ami aci	ino a id sing]	cids	3							

55

(ii) MOLECULE TYPE: protein

	(xi)	SEQ	JENC	E DES	SCRII	PTIO	N: SI	EQ II	NO:	5245	5:					
5	Asn 1	Pro	Ala	Leu	Thr 5	Val	Phe	Ala	Phe	Ile 10	Met	Ile	Ile	Ser	Ile 15	Leu
	Leu	Ala	Tyr	Val 20	Phe	Lys	Trp	Leu	Gly 25	Leu	Val	Asp	Asp	Val 30	Leu	Leu
10	Met	Val	Ile 35	Ile	Ile	Ser	Thr	Ile 40	Ser	Leu	Gly	Val	Val 45	Val	Pro	Thr
	Leu	Lys 50	Glu	Met	Asn	Ile	Met 55	Arg	Thr	Thr	Ile	Gly 60	Gln	Phe	Ile	Leu
15	Leu 65	Val	Ala	Val	Leu	Ala 70	Asp	Leu	Val	Thr	<b>Met</b> 75	Ile	Leu	Leu	Thr	Val 80
	Tyr	Gly	Ala	Ile	Asn 85	Gly	Gln	Gly	Gly	Ser 90	Thr	Ile	Trp	Leu	Ile 95	Gly
20	Ile	Leu	Val	Val 100	Phe	Thr	Ala	Ile	Ser 105	Tyr	Ile	Leu	Gly	Val 110	Gln	Phe
25	Lys	Arg	Met 115	Ser	Phe	Leu	Gln	Lys 120	Leu	Met	Asp	Gly	Thr 125	Thr	Gln	Ile
	Gly	Ile 130	Arg	Ala	Val	Phe	Ala 135	Leu	Ile	Ile	Leu	Leu 140	Val	Ala	Leu	Ala
30	Glu 145	Gly	Val	Gly	Ala	Glu 150	Asn	Ile	Leu	Gly	Ala 155	Phe	Leu	Ala	Gly	Val 160
	Val	Val	Ser	Leu	Leu 165	Asn	Pro	Asp	Glu	Glu 170	Met	Val	Glu	Lys	Leu 175	Asp
35	Ser	Phe	Gly	Tyr 180	Gly	Phe	Phe	Ile	Pro 185	Ile	Phe	Phe	Ile	<b>Me</b> t 190	Xaa	Gly
	Val	Asp	Leu 195	Asn	Ile	Pro	Ser	Leu 200		Lys	Glu	Pro	Lys 205	Leu	Leu	Ile
40	Ile	Ile 210	Pro	Ile	Leu	Ile	Val 215	Ala	Phe	Ile	Ile	Ser 220	Lys	Leu	Ile	Pro
45	Val 225	Met	Phe	Ile	Arg	Arg 230	Trp	Phe	Asp	Met	Lys 235	Thr	Thr	Ile	Ala	Ser 240
	Ala	Phe	Leu	Leu	Thr 245	Ser	Thr	Leu	Ser	<b>Leu</b> 250	Val	Ile	Ala	Ala	Ala 255	Lys
50	Ile	Ser	Glu	Arg 260	Leu	Asn	Ala	Ile	Ser 265	Ala	Glu	Thr	Ser	Gly 270	Ile	Leu
	Ile	Leu	Ser 275	Ala	Val	Ile	Thr	Cys 280	Val	Phe	Val	Pro	Ile 285	Ile	Phe	Lys
55	Lys	Leu 290	Phe	Pro	Val	Pro	Asp 295	Glu	Phe	Asn	Arg	300 Tàa	Ile	Glu	Val	Ser

		Leu 305	Ile	Gly	Lys	Asn	Gln 310	Leu	Thr	Ile	Pro	Ile 315	Ala	Gln	Asn	Leu	Thr 320
5		Ser	Gln	Leu	Tyr	Asp 325	Val	Thr	Leu	Tyr	Tyr 330	Arg	Lys	Asp	Leu	Ser 335	Asp
		Arg	Arg	Gln	Leu 340	Ser	Asp	Asp	Ile	Thr 345	Met	Ile	Glu	Ile	Ala 350	Asp	Tyr
10		Glu	Gln	<b>As</b> p 355	Val	Leu	Glu	Arg	Leu 360	Gly	Leu	Phe	Asp	Arg 365	Asp	Ile	Val
		Val	Cys 370	Ala	Thr	Asn	Asp	<b>Asp</b> 375	Asp	Ile	Asn	Arg	Lys 380	Val	Ala	Lys	Leu
15		Ala 385	Lys	Ala	His	Gln	Val 390	Glu	Arg	Val	Ile	Cys 395	Arg	Leu	Glu	Ser	Thr 400
20		Thr	Asp	Asp	Thr	Glu 405	Leu	Val	Asp	Ser	Gly 410	Ile	Glu	Ile	Phe	Ser 415	Ser
		Tyr	Leu	Ser	Asn 420	Lys	Ile	Leu	Leu	Lys 425	Gly	Leu	Ile	Glu	Thr 430	Pro	Asn
25		Met	Leu	Asn 435	Leu	Leu	Ser	Asn	Val 440	Glu	Thr	Ser	Leu	Tyr 445	Glu	Ile	Gln
		Met	Leu 450	Asn	Tyr	Lys	Tyr	Glu 455	Asn	Ile	Gln	Leu	<b>A</b> rg <b>4</b> 60	Asn	Phe	Pro	Phe
30		Gly 465	Gly	Asp	Ile	Ile											
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35		(i)	(A) (B) (C)	LEN TYP STF	GTH: PE: a PE: a	RACT 414 mino DNES Y: 1	ami aci SS: s	no a d ingl	cids	1							
40		(ii)	MOLE	CULE	TYP	E: p	rote	in									
45		(xi)	SEQU	JENCE	E DES	CRIF	TION	I: SE	II Q	NO:	5246	i :					
		Ala 1	Ile	Ile	Val	Ile 5	Leu	Leu	Phe	Leu	Arg 10	Asn	Ile	Arg	Thr	Thr 15	Ala
50		Ile	Ser	Ile	Ile 20	Ser	Ile	Pro	Leu	Ser 25	Leu	Leu	Met	Ala	<b>Le</b> u 30	Ile	Ala
		Leu	Lys	Leu 35	Ser	Asp	Val	Ser	Leu <b>4</b> 0	Asn	Ile	Leu	Thr	<b>Le</b> u 45	Gly	Ala	Leu
55		Thr	Val 50	Ala	Ile	Gly	Arg	Val 55	Ile	Asp	Asp	Ser	Ile 60	Val	Val	Val	Glu

	Asn 65	Ile	Tyr	Arg	Arg	Leu 70	Thr	Asp	Ser	Glu	Glu 75	Gln	Leu	Lys	Gly	Glu 80
5	Asn	Leu	Ile	Ile	Ser 85	Ala	Thr	Thr	Glu	Val 90	Phe	Lys	Pro	Ile	Met 95	Ser
	Ser	Thr	Leu	Val 100	Thr	Ile	Ile	Val	Phe 105	Leu	Pro	Leu	Val	Phe 110	Val	Ser
10	Gly	Ser	Val 115	Gly	Glu	Met	Phe	Arg 120	Pro	Phe	Ala	Leu	Ala 125	Ile	Ala	Phe
	Ser	Leu 130	Leu	Ala	Ser	Leu	Leu 135	Val	Ser	Ile	Thr	Leu 140	Val	Pro	Ala	Leu
15	Ala 145	Ala	Thr	Leu	Phe	<b>Lys</b> 150	Lys	Gly	Val	Lys	<b>Arg</b> 155	Arg	Asn	Lys	Gln	His 160
20	Gln	Glu	Gly	Leu	Gly 165	Val	Val	Ser	Thr	Thr 170	Tyr	Lys	Lys	Val	Leu 175	His
	Trp	Ser	Leu	Asn 180	His	ГÀЗ	Trp	Ile	Val 185	Ile	Ile	Leu	Ser	Thr 190	Leu	Ile
25	Leu	Val	Ala 195	Thr	Ile	Val	Phe	Gly 200	Gly	Pro	Arg	Leu	Gly 205	Thr	Ser	Phe
	Ile	Ser 210	Ala	Gly	Asp	Asp	Lys 215	Phe	Leu	Ala	Ile	Thr 220	Tyr	Thr	Pro	Lys
30	Pro 225	Gly	Glu	Thr	Glu	Gln 230	Ala	Val	Leu	Asn	His 235	Ala	Lys	Asp	Val	Glu 240
	Lys	Tyr	Leu	Lys	Gln 245	Lys	Lys	His	Val	Lys 250	Thr	Ile	Gln	Tyr	Ser 255	Val
35	Gly	Gly	Ser	Ser 260	Pro	Val	Asp	Pro	Thr 265	Gly	Ser	Thr	Asn	Ser 270	Met	Ala
	Ile	Met	Val 275	Glu	Tyr	Asp	Asn	Asp 280	Thr	Pro	Asn	Phe	Asp 285	Val	Glu	Ala
40	Asp	Lys 290	Val	Ile	Lys	His	Ala 295	Asp	Gly	Phe	Lys	His 300	Pro	Gly	Glu	Trp
45	Lys 305	Asn	Gln	Asp	Leu	Gly 310	Thr	Gly	Ala	Gly	Asn 315	Lys	Ser	Val	Glu	Val 320
	Thr	Val	Lys	Gly	Pro 325	Ser	Met	Asp	Ala	Ile 330	Lys	Ser	Thr	Val	Lys 335	Asp
50	Ile	Glu	Gln	Lys 340	Met	Lys	Gln	Val	Lys 345	Gly	Leu	Ala	Asn	Val 350	Lys	Ser
	Asp	Leu	Ser 355	Gln	Thr	Tyr	Asp	Gln 360	Tyr	Glu	Ile	Lys	Val 365	Asp	Gln	Asn
55	Lys	Ala 370	Ala	Glu	Asn	Gly	Ile 375	Ser	Ala	Ser	Gln	Leu 380	Ala	Met	His	Leu

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly 385 390 390 395

5		Lys	Thr	Val	Asp	Val 405	Lys	Val	Lys	Gln	Asn 410	Lys	Gln	Thr	Ala		
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10		(i)	(A) (B) (C)	LEI TYI	NGTH PE: a RANDI	: 559 amino EDNES	reris 5 am: 5 ac: 5S: 8	ino a id sing:	acid	9							
15		(ii)	MOL	ECULI	E TYI	PE: I	prote	ein									
20		(xi)	SEQ	JENCI	E DES	SCRII	PTIO	4: SI	EQ II	ONO:	524	7:					
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25		Thr	Thr	Ile	Leu 20	Phe	Gln	Tyr	Lys	Ile 25	Phe	Pro	Val	Leu	Met 30	Phe	Leu
		Val	Ser	Thr 35	Gly	Leu	Gly	Ile	Ile 40	Val	Ile	Thr	Gln	Asn 45	Ile	Leu	Ile
30		Ala	Asp 50	Phe	Leu	Ala	Lys	Ile 55	Ile	Arg	His	Gln	Phe 60	Gln	Gly	Leu	Trp
		Ile 65	Val	Leu	Phe	Ile	Leu 70	Leu	Gly	Val	Leu	Leu 75	Leu	Arg	Ala	Thr	Val 80
35		Gln	Phe	Leu	Asn	Gln 85	Trp	Leu	Gly	Asp	Thr 90	Leu	Ala	Phe	Lys	Val 95	Lys
		His	Met	Leu	Arg 100	Gln	Arg	Val	Ile	Tyr 105	Lys	Asn	Asn	Gly	His 110	Pro	Ile
40		Gly	Glu	Gln 115	Met				Thr 120				Asp	-	Leu	Ala	Pro
45		Phe	Tyr 130	Lys	Ser	Tyr	Leu	Pro 135	Gln	Val	Phe	Lys	Ser 140	Met	Met	Val	Pro
		Leu 145	Ile	Ile	Ile	Ile	<b>Ala</b> 150	Met	Phe	Phe	Ile	His 155	Phe	Asn	Thr	Ala	Leu 160
50		Ile	Met	Leu	Ile	Thr 165	Ala	Pro	Phe	Ile	Pro 170	Leu	Phe	Tyr	Ile	Ile 175	Phe
		Gly	Leu	Lys	Thr 180	Arg	Asp	Glu	Ser	Lys 185	Asp	Gln	Met	Thr	Tyr 190	Leu	Asn
55		Gln	Phe	Ser 195	Gln	Arg	Phe	Leu	Asn 200	Ile	Ala	Lys	Gly	<b>Le</b> u 205	Val	Thr	Leu

	Lys	210	Phe	Asn	Arg	Thr	215	Gin	Thr	Glu	Lys	H1S 220	He	Tyr	Asp	Asp
5	Ser 225	Thr	Gln	Phe	Arg	Thr 230	Leu	Thr	Met	Arg	Ile 235	Leu	Arg	Ser	Ala	Phe 240
	Leu	Ser	Gly	Leu	Met 245	Leu	Glu	Phe	Ile	<b>Ser</b> 250	Met	Leu	Gly	Ile	Gly 255	Leu
10	Val	Ala	Leu	Glu 260	Ala	Thr	Leu	Ser	Leu 265	Val	Val	Phe	His	Asn 270	Ile	Asp
	Phe	Lys	Thr 275	Ala	Ala	Ile	Ala	Ile 280	Ile	Leu	Ala	Pro	Glu 285	Phe	Tyr	Asn
15	Ala	Ile 290	Lys	Asp	Leu	Gly	Gln 295	Ala	Phe	His	Thr	Gly 300	Lys	Gln	Ser	Glu
20	Gly 305	Ala	Ser	Asp	Val	Val 310	Phe	Glu	Phe	Leu	Glu 315	Gln	Pro	Asn	Tyr	Asn 320
20	Asn	Glu	Phe	Leu	Leu 325	Lys	Tyr	Glu	Glu	Asn 330	Gln	Lys	Pro	Phe	11e 335	Gln
25	Leu	Thr	Asp	Ile 340	Ser	Phe	Arg	Tyr	Asp 345	Asp	Ser	Asp	Arg	Leu 350	Val	Leu
	Asn	Asp	Leu 355	Asn	Leu	Glu	Ile	Phe 360	Lys	Gly	Asp	Gln	Ile 365	Ala	Leu	Val
30	Gly	Pro 370	Ser	Gly	Ala	Gly	Lys 375	Ser	Thr	Leu	Thr	His 380	Leu	Ile	Ala	Gly
	Val 385	Tyr	Gln	Pro	Thr	Ile 390	Gly	Thr	Ile	Ser	Thr 395	Asn	Gln	Arg	Asp	Leu 400
35	Asn	Ile	Gly	Ile	Leu 405	Ser	Gln	Gln	Pro	Tyr 410	Ile	Phe	Ser	Ala	Ser 415	Ile
	Lys	Glu	Asn	Ile 420	Thr	Met	Phe	Lys	Asp 425	Ile	Glu	Asn	Asn	Thr.	Ile	Glu
40	Glu	Val	Leu 435	Asp	Glu	Val	Gly	Leu 440	Leu	Asp	ГÀз	Val	Gln 445	Ser	Phe	Thr
	Lys	Gly 450	Ile	Asn	Thr	Ile	Ile 455	Gly	Glu	Gly	Gly	Glu 460	Met	Leu	Ser	Gly
45	Gly 465	Gln	Met	Arg	Arg	Ile 470	Glu	Leu	Cys	Arg	Leu 475	Leu	Val	Met	Lys	Pro 480
50	Asp	Leu	Val	Ile	Phe 485	Asp	Glu	Pro	Ala	Thr 490	Gly	Leu	Asp	Ile	Gln 495	Thr
30	Glu	His	Met	Ile 500	Gln	Asn	Val	Leu	Phe 505	Gln	His	Phe	Lys	<b>Asp</b> 510	Thr	Thr
55	Met	Ile	Val 515	Ile	Ala	His	Arg	Asp 520	Asn	Thr	Ile	Arg	His 525	Leu	Gln	Arg

		Arg	<b>Le</b> u 530	Tyr	Ile	Glu	Asn	Gly 535	Arg	Leu	Ile	Ala	<b>Asp</b> 540	Asp	Arg	Asn	Ile
5		Ser 545	Val	Asn	Ile	Thr	Glu 550	Asn	Gly	Asp	Asp	<b>Le</b> u 555					
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10		(i)	(B)	LEI TYI	NGTH: PE: & RANDI	: 39: amino EDNES		ino a id sing:	acids	3							
15		(ii)	MOLE	ECULI	E TYI	PE: I	prot€	ein									
20		(xi)	SEQU	JENCI	E DES	SCRII	PTION	1: SI	EQ II	ONO:	: 5248	3:					
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25		Leu	Asn	Ser	Lys 20	Phe	Asn	Phe	Asn	Asn 25	Gly	ГÀЗ	Ile	Ala	Thr 30	Tyr	Leu
		Tyr	Lys	Glu 35	Arg	Thr	Ala	Met	Trp 40	Asn	Lys	Asn	Arg	Leu 45	Thr	Gln	Met
30		Leu	Ser 50	Ile	Glu	Tyr	Pro	Ile 55	Ile	Gln	Ala	Gly	Met 60	Ala	Gly	Ser	Thr
		Thr 65	Pro	Lys	Leu	Val	Ala 70	Ser	Val	Ser	Asn	Ser 75	Gly	Gly	Leu	Gly	Thr 80
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		Tyr	Val	Arg	Gln 100	Leu	Thr	Ser	Asn	Ser 105	Phe	Gly	Val	Asn	<b>Val</b> 110	Phe	Val
40		Pro	Ser	Gln 115	Gln	Ser	Tyr	Thr	Ser 120	Ser	Gln	Ile	Glu	Asn 125	Met	Asn	Ala
45		Trp	Leu 130	Lys	Pro	Tyr	Arg	<b>Arg</b> 135	Ala	Leu	His	Leu	Glu 140	Glu	Pro	Val	Val
45		Lys 145	Ile	Thr	Glu	Glu	Gln 150	Gln	Phe	Lys	Cys	His 155	Ile	Asp	Thr	Ile	Ile 160
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		Gln	Ile	Ile	Ser 180	Arg	Leu	Lys	Ala	Ala 185	Asn	Val	Lys	Leu	Ile 190	Gly	Thr
55		Ala	Thr	Ser 195	Val	Asp	Glu	Ala	Ile 200	Ala	Asn	Glu	Lys	Ala 205	Gly	Met	Asp

	Ala	11e 210	Val	Ala	Gln	GIÀ	215	Glu	Ala	Gly	GIÀ	H18 220	Arg	GIÀ	ser	Phe
5	Leu 225	Lys	Pro	Lys	Asn	Gln 230	Leu	Pro	Met	Val	Gly 235	Thr	Ile	Ser	Leu	Val 240
	Pro	Gln	Ile	Val	Asp 245	Val	Val	Ser	Ile	Pro 250	Val	Ile	Ala	Ala	Gly 255	Gly
10	Ile	Met	Asp	Gly 260	Arg	Gly	Val	Leu	Ala 265	Ser	Ile	Val	Leu	Gly 270	Ala	Glu
	Gly	Val	Gln 275	Met	Gly	Thr	Ala	Phe 280	Leu	Thr	Ser	Gln	Asp 285	Ser	Asn	Ala
15	Ser	Glu 290	Leu	Leu	Arg	Asp	Ala 295	Ile	Ile	Asn	Ser	Lys 300	Glu	Thr	Asp	Thr
20	<b>Val</b> 305	Ile	Thr	Lys	Ala	Phe 310	Ser	Gly	Lys	Leu	<b>Ala</b> 315	Arg	Gly	Ile	Asn	<b>Asn</b> 320
	Arg	Phe	Ile	Glu	Glu 325	Met	Ser	Gln	Tyr	Glu 330	Gly	Asp	Ile	Pro	<b>Asp</b> 335	Tyr
25	Pro	Ile	Gln	Asn 340	Glu	Leu	Thr	Ser	Ser 345	Ile	Arg	Lys	Ala	Ala 350	Ala	Asn
	Ile	Gly	Asp 355	Lys	Glu	Leu	Ile	His 360	Met	Trp	Ser	Gly	Gln 365	Ser	Pro	Arg
30	Leu	Ala 370	Thr	Thr	His	Pro	Ala 375	Asn	Thr	Ile	Met	Ser 380	Asn	Ile	Ile	Asn
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40	(ii)				GY: ] PE: ]											
45	(m. 2.)	0.00	·n		00D T	DOT O	v. C1	EO TI	a No	. 5341	n .					
	(xi)											Met	Lve	Lve	Lys	Glu
50	1	ASP	Pile	Leu	5 5	ALY	Gly	VOII	Lys	10	Adii	nec	Lys	БуЗ	15	Gru
	Lys	His	Ala	Ile 20	Arg	Lys	Lys	Ser	Ile 25	Gly	Val	Ala	Ser	Val 30	Leu	Val
55	Gly	Thr	Leu 35	Ile	Gly	Phe	Gly	Leu 40	Leu	Ser	Ser	Lys	Glu 45	Ala	Asp	Ala

	Ser	Glu 50	Asn	Ser	Val	Thr	Gln 55	Ser	Asp	Ser	Ala	Ser 60	Asn	Glu	Ser	Lys
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	Asn	Val	Ser	Asp	Thr 85	Lys	Thr	Ser	Ser	Asn 90	Thr	Asn	Asn	Gly	Glu 95	Thr
10	Ser	Val	Ala	Gln 100	Asn	Pro	Ala	Gln	Gln 105	Glu	Thr	Thr	Gln	Ser 110	Ser	Ser
	Thr	Asn	Ala 115	Thr	Thr	Glu	Glu	Thr 120	Pro	Val	Thr	Gly	Glu 125	Ala	Thr	Thr
15	Thr	Thr 130	Thr	Asn	Gln	Ala	Asn 135	Thr	Pro	Ala	Thr	Thr 140	Gln	Ser	Ser	Asn
20	Thr 145	Asn	Ala	Glu	Glu	<b>Le</b> u 150	Val	Asn	Gln	Thr	Ser 155	Asn	Glu	Thr	Thr	Ser 160
20	Asn	Asp	Thr	Asn	Thr 165	Val	Ser	Ser	Val	<b>As</b> n 170	Ser	Pro	Gln	Asn	Ser 175	Thr
25	Asn	Ala	Glu	<b>As</b> n 180	Val	Ser	Thr	Thr	Gln 185	Asp	Thr	Ser	Thr	Glu 190	Ala	Thr
	Pro	Ser	Asn 195	Asn	Glu	Ser	Ala	Pro 200	Gln	Ser	Thr	Asp	Ala 205	Ser	Asn	Lys
30	Asp	Val 210	Val	Asn	Gln	Ala	Val 215	Asn	Thr	Ser	Ala	Pro 220	Arg	Met	Arg	Ala
	Phe 225	Ser	Leu	Ala	Ala	Val 230	Ala	Ala	Asp	Ala	Pro 235	Val	Ala	Gly	Thr	Asp 240
35	Ile	Thr	Asn	Gln	Leu 245	Thr	Asn	Val	Thr	Val 250	Gly	Ile	Asp	Ser	Gly 255	Thr
	Thr	Val	Tyr	Pro 260	His	Gln	Ala	Gly	Tyr 265	Val	Lys	Leu	Asn	Tyr 270	Gly	Phe
40	Ser	Val	Pro 275	Asn	Ser	Ala	Val	Lys 280	Gly	Asp	Thr	Phe	Lys 285	Ile	Thr	Val
46	Pro	Lys 290	Glu	Leu	Asn	Leu	<b>Asn</b> 295	Gly	Val	Thr	Ser	Thr 300	Ala	Lys	Val	Pro
45	Pro 305	Ile	Met	Ala	Gly	Asp 310	Gln	Val	Leu	Ala	Asn 315	Gly	Val	Ile	Asp	Ser 320
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	Asp	Val	Lys	Ala 340	Thr	Leu	Thr	Met	Pro 345	Ala	Tyr	Ile	Asp	Pro 350	Glu	Asn
55	Val	Lys	Lys 355	Thr	Gly	Asn	Val	Thr 360	Leu	Ala	Thr	Gly	11e 365	Gly	Ser	Thr

	Thr	Ala 370	Asn	Lys	Thr	Val	Leu 375	Val	Asp	Tyr	Glu	Lys 380	Tyr	Gly	Lys	Phe
5	Tyr 385	Asn	Leu	Ser	Ile	<b>Lys</b> 390	Gly	Thr	Ile	Ąsp	Gln 395	Ile	Asp	Lys	Thr	Asn 400
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10	Ile	Ala	Pro	Val 420	Leu	Thr	Gly	Asn	Leu 425	Lys	Pro	Asn	Thr	Asp 430	Ser	Asn
	Ala	Leu	Ile 435	Asp	Gln	Gln	Asn	Thr 440	Ser	Ile	Lys	Val	Tyr 445	Lys	Val	Asp
15	Asn	Ala 450	Ala	Asp	Leu	Ser	Glu 455	Ser	Tyr	Phe	Val	Asn 460	Pro	Glu	Asn	Phe
	Glu 465	Asp	Val	Thr	Asn	Ser 470	Val	Asn	Ile	Thr	Phe 475	Pro	Asn	Pro	Asn	Gln 480
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25	Ile	Val	Val	Val 500	Asn	Gly	His	Ile	<b>As</b> p 505	Pro	Asn	Ser	Lys	Gly 510	Asp	Leu
	Ala	Leu	Arg 515	Ser	Thr	Leu	Tyr	Gly 520	Tyr	Asn	Ser	Asn	Ile 525	Ile	Trp	Arg
30	Ser	Met 530	Ser	Trp	Asp	Asn	Glu 535	Val	Ala	Phe	Asn	<b>As</b> n 540	Gly	Ser	Gly	Ser
	Gly 545	Asp	Gly	Ile	Asp	<b>Lys</b> 550	Pro	Val	Val	Pro	Glu 555	Gln	Pro	Asp	Glu	Pro 560
35	Gly	Glu	Ile	Glu	Pro 565	Ile	Pro	Glu	Asp	Ser 570	Asp	Ser	Asp	Pro	Gly 575	Ser
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40	Asp	Ser	Thr 595	Ser	Asp	Ser	Gly	Ser 600	Asp	Ser	Ala	Ser	Asp 605		Asp	Ser
	Ala	Ser 610	Asp	Ser	Asp	Ser	Ala 615		qeA	Ser	Asp	Ser 620	Ala	Ser	Asp	Ser
45	<b>As</b> p 625	Ser	Ala	Ser	Asp	Ser 630		Ser	Asp	Asn	<b>As</b> p 635	Ser	Asp	Ser	Asp	Ser 640
50	Asp	Ser	Asp	Ser	<b>Asp</b> 645	Ser	Asp	Ser	Asp	Ser 650	Asp	Ser	Asp	Ser	<b>Asp</b> 655	Ser
50	Asp	Ser	Asp	Ser 660		Ser	Asp	Ser	Asp 665		Asp	Ser	Asp	Ser 670	Asp	Ser
55	Asp	Ser	<b>As</b> p 675		Asp	Ser	Asp	Ser 680	Asp	Ser	Asp	Ser	Asp 685	Ser	Asp	Ser

		Asp	Ser 690	Asp	Ser	Asp	Ser	<b>As</b> p 695	Ser	Asp	Ser	Asp	Ser 700	Asp	Ser	Asp	Ser
5		Asp 705	Ser	Asp	Ser	Asp	Ser 710	Asp	Ser	Asp	Ser	<b>Asp</b> 715	Ser	Asp	Ser	Asp	Ser 720
		Asp	Ser	Asp	Ser	<b>Asp</b> 725	Ser	Asp	Ser	Asp	Ser 730	Asp	Ser	Asp	Ser	<b>Asp</b> 735	Ser
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		Asp	Ser 770	Asp	Ser	Asp	Ser	<b>Asp</b> 775	Ser	Ala	Ser	Asp	Ser 780	Asp	Ser	Asp	Ser
20		<b>Asp</b> 785	Ser	Asp	Ser	Asp	Ser 790	Asp	Ser	Asp	Ser	<b>Asp</b> 795	Ser	Asp	Ser	Asp	Ser 800
		Asp	Ser	Asp	Ser	<b>Asp</b> 805	Ser	Asp	Ser	Asp	Ser 810	Asp	Ser	Asp	Ser	<b>As</b> p 815	Ser
25		Glu	Ser	Asp	<b>Ser</b> 820	Asp	Ser	Asp	Ser	<b>Asp 82</b> 5	Ser	Asp	Ser	Asp	Ser 830	Asp	Ser
		Asp	Ser	Asp 835	Ser	Asp	Ser	Asp	Ser 840	Ala	Ser	Asp	Ser	<b>Asp</b> 845	Ser	Gly	Ser
30		Asp	<b>Ser</b> 850	Asp	Ser	Ser	Ser	<b>As</b> p 855	Ser	Asp	Ser	Glu	<b>Ser</b> 860	Asp	Ser	Asn	Ser
35		<b>Asp</b> <b>86</b> 5	Ser	Glu	Ser	Val	Ser 870	Asn	Asn	Asn	Val	Val 875	Pro	Pro	Asn	Ser	Pro 880
		Lys	Asn	Gly	Thr	Asn 885	Ala	Ser	Asn	Lys	<b>As</b> n 890	Glu	Ala	Lys	Asp	Ser 895	Lys
40		Glu	Pro	Leu	Pro 900		Thr	Gly		Glu 905		Glu	Ala	Asn	Thr 910	Ser	Leu
		Ile	Trp	Gly 915	Leu	Leu	Ala	Ser	Ile 920	Gly	Ser	Leu	Leu	<b>Le</b> u 925	Phe	Arg	Arg
45		Lys	Lys 930	Glu	Asn	Lys	Asp	Lys 935	Lys								
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50		(i)	(B) (C)	LEN TYP	IGTH: PE: & RANDE	ARACT 194 amino EDNES SY: 1	lami aci SS: s	ino a id singl	cids	5							
55		1223						,									

(ii) MOLECULE TYPE: protein

	(xi)	SEQ	UENCI	E DES	SCRI	PTIO	N: SI	EQ II	ONO:	:5250	):					
5	Val 1	Ser	Lys	Leu	Lys 5	Lys	Glu	Ile	Leu	Glu 10	Trp	Ile	Ile	Ser	Ile 15	Ala
	Val	Ala	Phe	Val 20	Ile	Leu	Phe	Ile	Val 25	Gly	Lys	Phe	Ile	Val 30	Thr	Pro
10	Tyr	Thr	Ile 35	Lys	Gly	Glu	Ser	Met 40	Asp	Pro	Thr	Leu	Lys 45	Asp	Gly	Glu
	Arg	Val 50	Ala	Val	Asn	Ile	Val 55	Gly	Tyr	Lys	Thr	Gly 60	Gly	Leu	Glu	Lys
15	Gly 65	Asn	Val	Val	Val	Phe 70	His	Ala	Asn	Lys	Asn 75	qeA	Asp	Tyr	Val	Lys 80
	Arg	Val	Ile	Gly	Val 85	Pro	Gly	<b>As</b> p	Lys	<b>Val</b> 90	Glu	Tyr	Lys	Asn	Asp 95	Thr
20	Leu	Tyr	Val	Asn 100	Gly	Lys	Lys	Gln	Asp 105	Glu	Pro	Tyr	Leu	Asn 110	Tyr	Asn
25	Leu	Lys	His 115	Lys	Gln	Gly	Asp	Tyr 120	Ile	Thr	Gly	Thr	Phe 125	Gln	Val	Lys
	Asp	Leu 130	Pro	Asn	Ala	Asn	Pro 135	Lys	Ser	Asn	Val	Ile 140	Pro	Lys	Gly	Lys
30	Tyr 145	Leu	Val	Leu	Gly	<b>Asp</b> 150	Asn	Arg	Glu	Val	Ser 155	Lys	Asp	Ser	Arg	Ala 160
	Phe	Gly	Leu	Ile	Asp 165	Glu	Asp	Gln	Ile	Val 170	Gly	Lys	Val	Ser	Phe 175	Gln
35	Val	Leu	Ala	His 180	Phe	Ser	Glu	Phe	Gln 185	Thr	Ser	Ile	Ser	Xaa 190	Leu	Lys
	Ile	Leu														
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45	(i)	(A) (B) (C)	LEI TYI STI	NGTH PE: 8 RANDI	: 559 amino EDNES	reris 9 am: 5 ac: 5S: 8	ino a id singl	acids	3							
	(ii)	MOL	ECULI	E TYI	PE: I	prote	ein									
50																
	(xi)	SEQ	UENC	E DES	SCRII	PTIO	1: SI	EQ II	ON C	525	L:					
55	Leu 1	Lys	Ala	Xaa	Tyr 5	Ala	Lys	Leu	Asp	Asp 10	Val	Ser	Lys	Phe	Glu 15	Asp

	Val	Thr	Asp	Asn 20	Met	Ser	Leu	Asp	Phe 25	Asp	Thr	Asn	Gly	Gly 30	Tyr	Ser
5	Leu	Asn	Phe 35	Asn	Asn	Leu	Asp	Gln 40	Ser	Lys	Asn	Tyr	Val 45	Ile	Lys	Tyr
	Glu	Gly 50	Tyr	Tyr	Asp	Ser	Asn 55	Ala	Ser	Asn	Leu	Glu 60	Phe	Gln	Thr	His
10	Leu 65	Phe	Gly	Tyr	Tyr	Asn 70	Tyr	Tyr	Tyr	Thr	Ser 75	Asn	Leu	Thr	Trp	Lys 80
45	Asn	Gly	Val	Ala	Phe 85	Tyr	Ser	Asn	Asn	Ala 90	Gln	Gly	Asp	Gly	Lys 95	Asp
15	Lys	Leu	Lys	Glu 100	Pro	Ile	Ile	Glu	His 105	Ser	Thr	Pro	Ile	Glu 110	Leu	Glu
20	Phe	Lys	Ser 115	Glu	Pro	Pro	Val	Glu 120	Lys	His	Glu	Leu	Thr 125	Gly	Thr	Ile
	Glu	Glu 130	Ser	Asn	Asp	Ser	Lys 135	Pro	Ile	Asp	Phe	Glu 140	Tyr	His	Thr	Ala
25	Val 145	Glu	Gly	Ala	Glu	Gly 150	His	Ala	Glu	Gly	Thr 155	Ile	Glu	Thr	Glu	Glu 160
	Asp	Ser	Ile	His	Val 165	Asp	Phe	Glu	Glu	Ser 170	Thr	His	Glu	Asn	Ser 175	Lys
30	His	His	Ala	Asp 180	Val	Val	Glu	Tyr	Glu 185	Glu	Asp	Thr	Asn	Pro 190	Gly	Gly
	Gly	Gln	Val 195	Thr	Thr	Glu	Ser	Asn 200	Leu	Val	Glu	Phe	Asp 205	Glu	Asp	Ser
35	Thr	Lys 210	Gly	Ile	Val	Thr	Gly 215	Ala	Val	Ser	Asp	His 220	Thr	Thr	Ile	Glu
40	Asp 225	Thr	Lys	Glu	Tyr	Thr 230	Thr	Glu	Ser	Asn	Leu 235	Ile	Glu	Leu	Val	Asp 240
40	Glu	Leu	Pro	Glu	Glu 245	His	Gly	Gln	Ala	Gln 250	Gly	Pro	Ile	Glu	Glu 255	Ile
45	Thr	Glu	Asn	<b>Asn</b> 260	His	His	Ile	Ser	His 265	Ser	Gly	Leu	Gly	Thr 270	Glu	Asn
	Gly	His	Gly 275	Asn	Tyr	Gly	Val	Ile 280	Glu	Glu	Ile	Glu	Glu 285	Asn	Ser	His
50	Val	<b>Asp</b> 290	Ile	Lys	Ser	Glu	<b>Leu</b> 295	Gly	Tyr	Glu	Gly	Gly 300	Gln	Asn	Ser	Gly
	Asn 305	Gln	Ser	Phe	Glu	Glu 310	Asp	Thr	Glu	Glu	<b>Asp</b> 315	Lys	Pro	Lys	Tyr	Glu 320
55	Gln	Gly	Gly	Asn	Ile 325	Val	qaA	Ile	Asp	Phe 330	Asp	Ser	Val	Pro	Gln 335	Ile

	His	Gly	Gln	Asn 340	Asn	Gly	Asn	Gln	Ser 345	Phe	Glu	Glu	Asp	Thr 350	Glu	Lys
5	Asp	Lys	Pro 355	Lys	Tyr	Glu	Gln	Gly 360	Gly	Asn	Ile	Ile	<b>Asp</b> 365	Ile	Asp	Phe
	Asp	Ser 370	Val	Pro	His	Ile	His 375	Gly	Phe	Asn	Lys	His 380	Thr	Glu	Ile	Ile
10	Glu 385	Glu	Asp	Thr	Asn	Lys 390	Asp	Lys	Pro	Asn	Tyr 395	Gln	Phe	Gly	Gly	His 400
	Asn	Ser	Val	Asp	Phe 405	Glu	Glu	Asp	Thr	<b>Leu</b> <b>41</b> 0	Pro	Gln	Val	Ser	Gly 415	His
15	Asn	Glu	Gly	Gln 420	Gln	Thr	Ile	Glu	Glu <b>42</b> 5	Asp	Thr	Thr	Pro	Pro 430	Ile	Val
20	Pro	Pro	Thr 435	Pro	Pro	Thr	Pro	Glu 440	Val	Pro	Ser	Glu	Pro 445	Glu	Thr	Pro
	Thr	Pro 450	Pro	Thr	Pro	Glu	Val 455	Pro	Ser	Glu	Pro	Glu <b>46</b> 0	Thr	Pro	Thr	Pro
25	Pro 465	Thr	Pro	Glu	Val	Pro 470	Thr	Glu	Pro	Gly	Lys 475	Pro	Ile	Pro	Pro	Ala 480
	Lys	Glu	Glu	Pro	Lys 485	Lys	Pro	Ser	Lys	Pro 490	Val	Glu	Gln	Gly	<b>Lys</b> 495	Val
30	Val	Thr	Pro	<b>Val</b> 500	Ile	Glu	Ile	Asn	Glu 505	Lys	Val	Lys	Ala	<b>Val</b> 510	Val	Pro
	Thr	Lys	Lys 515	Ala	Gln	Ser	Lys	<b>Lys</b> 520	Ser	Glu	Leu	Pro	Glu 525	Thr	Gly	Gly
35	Glu	Glu 530	Ser	Thr	Asn	Asn	Gly 535	Met	Leu	Phe	Gly	Gly 540	Leu	Phe	Ser	Ile
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	(ii)	MOLE	CULE	E TYI	PE: p	rote	ein									
50																
	(xi)	SEQU	ENCE	E DES	SCRIE	OITS	1: SE	EQ II	NO:	5252	2:					
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	Val	Val	Glu	Glu 20	Thr	Lys	Ala	Thr	Gly 25	Thr	Asp	Val	Thr	Asn 30	Lys	Val
5	Glu	Val	Glu 35	Glu	Gly	Ser	Glu	Ile 40	Val	Gly	His	Lys	Gln 45	Asp	Thr	Asn
	Val	Val 50	Asn	Pro	His	Asn	Ala 55	Glu	Arg	Val	Thr	Leu 60	Lys	Tyr	Lys	Trp
10	Lys 65	Phe	Gly	Glu	Gly	Ile 70	Lys	Ala	Gly	Asp	Tyr 75	Phe	Asp	Phe	Thr	Leu 80
	Ser	Asp	Asn	Val	Glu 85	Thr	His	Gly	Ile	Ser 90	Thr	Leu	Arg	Lys	Val 95	Pro
15	Glu	Ile	Lys	<b>Ser</b> 100	Thr	Ąsp	Gly	Gln	<b>Val</b> 105	Met	Ala	Thr	Gly	Glu 110	Ile	Ile
20	Gly	Glu	Arg 115	Lys	Val	Arg	Tyr	Thr 120	Phe	Lys	Glu	Tyr	<b>Val</b> 125	Gln	Glu	Lys
	Lys	Asp 130	Leu	Thr	Ala	Glu	Leu 135	Ser	Leu	Asn	Leu	Phe 140	Ile	Asp	Pro	Thr
25	Thr 145	Val	Thr	Gln	Lys	Gly 150	Asn	Gln	Asn	Val	Glu 155	Val	Lys	Leu	Gly	Glu 160
	Thr	Thr	Val	Ser	Lys 165	Ile	Phe	Asn	Ile	Gln 170	Tyr	Leu	Gly	Gly	Val 175	Arg
30	Asp	Asn	Trp	Gly 180	Val	Thr	Ala	Asn	Gly 185	Arg	Ile	Asp	Thr	Leu 190	Asn	Lys
	Val	Asp	Gly 195	Lys	Phe	Ser	His	Phe 200	Ala	Tyr	Met	Lys	Pro 205	Asn	Asn	Gln
35	Ser	Leu 210	Ser	Ser	Val	Thr	Val 215	Thr	Gly	Gln	Val	Thr 220	ГЛЗ	Gly	Asn	Lys
	Pro 225	Gly	Val	Asn	Asn	Pro 230	Thr	Val	Lys	Val	Tyr 235	Lys	His	Ile	Gly	Ser 240
40	Asp	Asp	Leu	Ala	Glu 245	Ser	Xaa	Xaa	Cys	Lys 250	Ala					
(2)	INFOR	TAMS	ON F	OR S	SEQ I	D NC	525	3:								
45	(i)	(B) (C)	LEN TYP	IGTH: PE: a RANDE	163 minc DNES	ami aci SS: s	ino a id singl	cids	3							
50	(ii)	MOLE	CULE	TYF	E: p	rote	ein									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

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5		Gly	Ile	Arg	Lys 20	His	Lys	Leu	Gly	Ala 25	Ala	Ser	Val	Phe	Leu 30	Gly	Thr
		Met	Ile	Val 35	Val	Gly	Met	Gly	Gln 40	Glu	Lys	Glu	Ala	Ala 45	Ala	Ser	Glu
10		Gln	Asn 50	Asn	Thr	Thr	Val	Glu 55	Glu	Ser	Gly	Ser	Ser 60	Ala	Thr	Glu	Ser
		Lys 65	Ala	Ser	Glu	Thr	Gln 70	Thr	Thr	Thr	Asn	Asn 75	Val	Asn	Thr	Ile	Asp 80
15		Glu	Thr	Gln	Ser	Tyr 85	Ser	Ala	Thr	Ser	Thr 90	Glu	Gln	Pro	Ser	Gln 95	Ser
20		Thr	Gln	Val	Thr 100	Thr	Glu	Glu	Ala	Pro 105	Lys	Thr	Val	Gln	Ala 110	Pro	Lys
		Val	Glu	Thr 115	Ser	Arg	Val	Asp	Leu 120	Pro	Ser	Glu	Lys	Val 125	Ala	qaA	ГÀЗ
25		Glu	Thr 130	Thr	Gly	Thr	Gln	Val 135	Asp	Ile	Ala	Gln	Pro 140	Ser	Asn	Val	Ser
		Glu 145	Ile	Lys	Pro	Arg	<b>Met</b> 150	Lys	Arg	Ser	Met	Thr 155	Leu	Gln	Gln	Leu	Gln 160
30		Arg	Lys	Lys													
	(2)	INFOR	TAMS	ION I	FOR S	SEQ :	ID NO	525	54:								
35		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 8 RAND	: 102 amino EDNES	TERIS  27 ar  5 ac:  5S: s  lines	nino ld sing:	acio	is							
40		(ii)	MOLI	ECULI	E TY	PE: 1	prote	ein									
45		(xi)	SEQ	UENCI	E DE	SCRI	PTIO	N: S	EQ II	ON O	:525	4:					
43		Ile 1	Leu	His	Leu	Lys 5	Gly	Asp	Ile	Ile	Val 10	Lys	Asn	Asn	Leu	Arg 15	Tyr
50		Gly	Ile	Arg	Lys 20	His	Lys	Leu	Gly	Ala 25	Ala	Ser	Val	Phe	Leu 30	Gly	Thr
		Met	Ile	Val 35	Val	Gly	Met	Gly	Gln 40	Asp	Lys	Glu	Ala	Ala 45	Ala	Ser	Glu
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	Lys 65	Thr	Ser	Glu	Thr	Gln 70	Thr	Thr	Ala	Thr	Asn 75	Val	Asn	His	Ile	Glu 80
5	Glu	Thr	Gln	Ser	Tyr 85	Asn	Ala	Thr	Val	Thr 90	Glu	Gln	Pro	Ser	Asn 95	Ala
	Thr	Gln	Val	Thr 100	Thr	Glu	Glu	Ala	Pro 105	Lys	Ala	Val	Gln	Ala 110	Pro	Gln
10	Thr	Ala	Gln 115	Pro	Ala	Asn	Ile	Glu 120	Thr	Val	ГÀЗ	Glu	Glu 125	Val	Val	Lys
	Glu	Glu 130	Ala	Lys	Pro	Gln	Val 135	Lys	Glu	Thr	Thr	Gln 140	Ser	Gln	Asp	Asn
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25	ГÀЗ	Glu	Ala 195	Ser	Asn	Ala	Lys	Val 200	Glu	Thr	Gly	Thr	Asp 205	Val	Thr	Ser
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30	Lys 225	Val	Glu	Pro	His	Ala 230	Gly	Gln	Arg	Ala	Val 235	Leu	Lys	Tyr	Lys	Leu 240
	Lys	Phe	Glu	Asn	Gly 245	Leu	His	Gln	Gly	<b>As</b> p 250	Tyr	Phe	Asp	Phe	Thr 255	Leu
35	Ser	Asn	Asn	Val 260	Asn	Thr	His	Gly	Val 265	Ser	Thr	Ala	Arg	Lys 270	Val	Pro
	Glu	Ile	Lys 275	Asn	Gly	Ser	Val	Val 280	Met	Ala	Thr	Gly	Glu 285	Val	Leu	Glu
40	Gly	Gly 290	Lys	Ile	Arg	Tyr	Thr 295	Phe	Thr	Asn	Asp	Ile 300	Glu	Asp	Lys	Val
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55	Asn	Arg 370	Phe	Ser	His	Val	Ala 375	Phe	Ile	Lys	Pro	Asn 380	Asn	Gly	Lys	Thr

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5	Gly	Asn	Gln	Pro	Lys 405	Val	Arg	Ile	Phe	Glu 410	Tyr	Leu	Gly	Asn	<b>As</b> n 415	Glu
	Asp	Ile	Ala	Lys 420	Ser	Val	Tyr	Ala	Asn 425	Thr	Thr	Asp	Thr	Ser 430	Lys	Phe
0	Lys	Glu	Val 435	Thr	Ser	Asn	Met	Ser 440	Gly	Asn	Leu	Asn	Leu 445	Gln	Asn	Asn
	Gly	<b>Ser</b> <b>4</b> 50	Tyr	Ser	Leu	Asn	Ile 455	Glu	Asn	Leu	Asp	Lys 460	Thr	Tyr	Val	Val
5	His 465	Tyr	Asp	Gly	Glu	Tyr 470	Leu	Asn	Gly	Thr	<b>Asp</b> 475	Glu	Val	Asp	Phe	Arg 480
_	Thr	Gln	Met	Val	Gly 485	His	Pro	Glu	Gln	Leu 490	Tyr	Lys	Tyr	Tyr	Tyr 495	Asp
20	Arg	Gly	Tyr	Thr 500	Leu	Thr	Trp	Asp	<b>As</b> n 505	Gly	Leu	Val	Leu	<b>Tyr</b> 510	Ser	Asn
25	Lys	Ala	<b>As</b> n 515	Gly	Asn	Glu	Lys	Asn 520	Gly	Pro	Ile	Ile	Gln 525	Asn	Asn	Lys
	Phe	Glu 530	Tyr	Lys	Glu	Asp	Thr 535	Ile	Lys	Glu	Thr	Leu 540	Thr	Gly	Gln	Tyr
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	Leu	Asp	Ile	Asp	Tyr 565	His	Thr	Ala	Ile	Asp 570	Gly	Gly	Gly	Gly	<b>Tyr</b> 575	Val
35	Asp	Gly	Tyr	Ile 580	Glu	Thr	Ile	Glu	Glu 585	Thr	Asp	Ser	Ser	Ala 590	Ile	Asp
	Ile	Asp	Tyr 595	His	Thr	Ala	Val	<b>Asp</b> 600	Ser	Glu	Ala	Gly	His 605	Val	Gly	Gly
40	Tyr	Thr 610	Glu	Ser	Ser	Glu	Glu 615	Ser	Asn	Pro	Ile	<b>Asp</b> 620	Phe	Glu	Glu	Ser
	Thr 625	His	Glu	Asn	Ser	630	His	His	Ala	Asp	<b>Val</b> 635	Val	Glu	Tyr	Glu	Glu 640
45	Asp	Thr	Asn	Pro	Gly 645		Gly	Gln	Val	Thr 650		Glu	Ser	Asn	Leu 655	Val
50	Glu	Phe	Asp	Glu 660		Ser	Thr	Lys	Gly 665	Ile	Val	Thr	Gly	Ala 670		Ser
	Asp	His	Thr 675		Val	Glu	Asp	Thr 680		Glu	Tyr	Thr	Thr 685		Ser	Asn
55	Leu	Ile 690		Leu	Val	Asp	Glu 695		Pro	Glu	Glu	His		Gln	Ala	Gln

	Gly 705	Pro	Val	Glu	Glu	Ile 710	Thr	Lys	Asn	Asn	His 715	His	Ile	Ser	His	<b>Ser</b> 720
5	Gly	Leu	Gly	Thr	Glu 725	Asn	Gly	His	Gly	<b>As</b> n <b>73</b> 0	Tyr	Asp	Val	Ile	Glu 735	Glu
	Ile	Glu	Glu	<b>Asn</b> 740	Ser	His	Val	Asp	Ile 745	Lys	Ser	Glu	Leu	Gly 750	Tyr	Glu
10	Gly	Gly	Gln 755	Asn	Ser	Gly	Asn	Gln 760	Ser	Phe	Glu	Glu	Asp 765	Thr	Glu	Glu
	qsA	Lys 770	Pro	Lys	Tyr	Glu	Gln 775	Gly	Gly	Asn	Ile	Val 780	Asp	Ile	Asp	Phe
15	<b>Asp</b> 785	Ser	Val	Pro	Gln	Ile 790	His	Gly	Gln	Asn	Lys 795	Gly	Asn	Gln	Ser	Phe 800
20	Glu	Glu	Asp	Thr	Glu 805	Lys	Asp	Lys	Pro	Lys 810	Tyr	Glu	His	Gly	Gly 815	Asn
	Ile	Ile	Asp	Ile 820	Asp	Phe	Asp	Ser	<b>Val</b> 825	Pro	His	Ile	His	Gly 830	Phe	Asn
25	Lys	His	Thr 835	Glu	Ile	Ile	Glu	Glu 840	Asp	Thr	Asn	Lys	Asp 845	Lys	Pro	Ser
	Tyr	Gln 850	Phe	Gly	Gly	His	Asn 855	Ser	Val	Asp	Phe	Glu 860	Glu	Asp	Thr	Leu
30	Pro 865	Lys	Val	Ser	Gly	Gln 870	Asn	Glu	Gly	Gln	Gln 875	Thr	Ile	Glu	Glu	<b>Asp</b> 880
	Thr	Thr	Pro	Pro	Ile 885	Val	Pro	Pro	Thr	Pro 890	Pro	Thr	Pro	Glu	Val 895	Pro
35	Ser	Glu	Pro	Glu 900	Thr	Pro	Thr	Pro	Pro 905	Thr	Pro	Glu	Val	Pro 910	Ser	Glu
	Pro	Glu	Thr 915	Pro	Thr	Pro	Pro	Thr 920	Pro	Glu	Val	Pro	<b>Ser</b> 925	Glu.	Pro	Glu
40	Thr	Pro 930	Thr	Pro	Pro	Thr	Pro 935	Glu	Val	Pro	Ala	Glu 940	Pro	Gly	Lys	Pro
45	Val 945	Pro	Pro	Ala	Lys	Glu 950	Glu	Pro	Lys	Lys	Pro 955	Ser	Lys	Pro	Val	Glu 960
	Gln	Gly	Lys	Val	Val 965	Thr	Pro	Val	Ile	Glu 970	Ile	Asn	Glu	Lys	<b>Val</b> 975	Lys
50	Ala	Val	Ala	Pro 980	Thr	Lys	Lys	Pro	Gln 985	Ser	Lys	Lys	Ser	Glu 990	Leu	Pro
	Glu	Thr	Gly 995	Gly	Glu	Glu	Ser	Thr 1000		Lys	Gly	Met	Leu 1009		Gly	Gly
55	Leu	Phe 1010		Ile	Leu	Gly	Leu 1015		Leu	Leu	Arg	Arg 1020		Lys	Lys	Asn

His Lys Ala 1025

- (2) INFORMATION FOR SEQ ID NO:5255:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:
- Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
  1 5 10 15
  - Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu 20 25 30
  - Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys 35 40 45
  - Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp 50 55 60
  - Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu 65 70 75 80
  - Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val 85 90 95
  - Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
    100 105 110
  - Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys 115 120 125
  - Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys 130 135 140
  - Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg 145 150 155

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#### Claims

- Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
- 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

- 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
  - 5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
    - (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS: 1-5,191;
    - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
    - (c) retrieval means for obtaining said homologous sequence(s) of step (b).
  - 6. A method for identifying commercially important nucleic acid fragments of the Staphylococcus aureus genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected
  - 7. A method for identifying an expression modulating fragment of Staphylococcus aureus genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
- **8.** A protein-encoding nucleic acid fragment of the Staphylococcus aureus genome, wherein said fragment comprises the nucleotide sequence of any one of the

wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS. 1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.

9. The nucleic acid fragment of claim 8 which is DNA.

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- 10. The nucleic acid fragment of claim 8 which is RNA.
- 11. A vector comprising a fragment of claim 8
- 12. A fragment of the Staphylococcus aureus genome, wherein said fragment modulates the expression of an operably liked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 13. A vector comprising a fragment of claim 12.
- 14. A organism which has been altered to contain any one of the fragments of the Staphylococcus aureus genome of claim 8.
  - 15. A method for producing a polypeptide in a host cell comprising the steps of:
    - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
    - (b) isolating said protein.
  - 16. An organism which has been altered to contain any one of the fragments of the Staphylococcus aureus genome

of claim 12.

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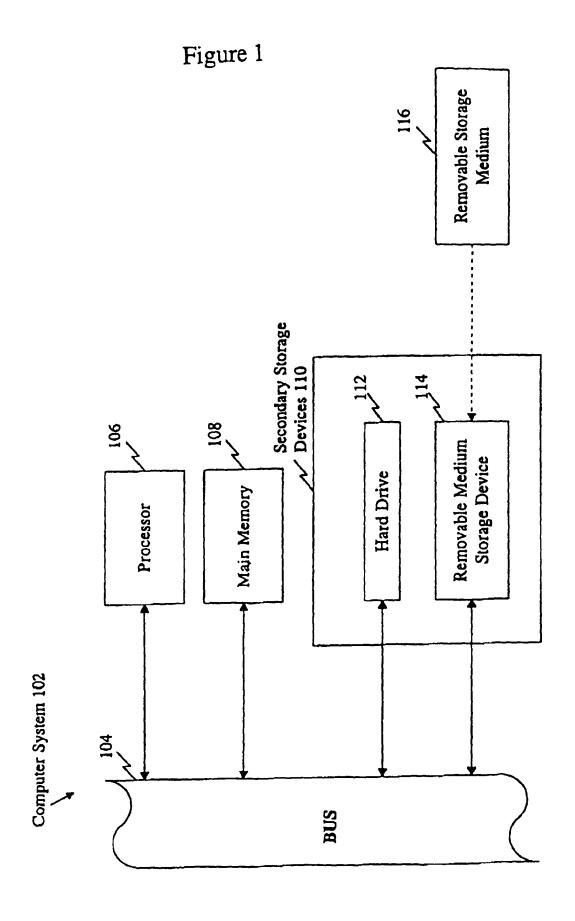
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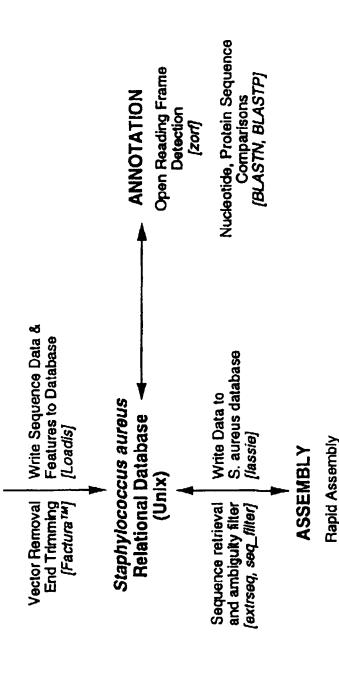
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- 17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the Staphylococcus aureus genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 18. A nucleic acid molecule being a homolog of any of the fragments of the Staphylococcus aureus genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5.191 and Tables 2 and 3, including fragments thereof;
  - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
  - (c) isolating the nucleic acid molecules from said members identified in step (b).
- 19. A DNA molecule being a homolog of any one of the fragments of the Staphylococcus aureus genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) isolating mRNA, DNA, or cDNA produced from an organism;
  - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
  - (c) isolating said amplified sequences produced in step (b).
- 20. A polypeptide encoded by a fragment of claim 8.
- 21. An antibody which selectively binds to any one of the polypeptides of claim 20.
- 22. A kit for analyzing samples for the presence of polynucleotides derived from Staphylococcus aureus, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a staphylococcus aureus polynucleotide under stringent hybridization conditions, and a suitable container.
- 23. A Staphylococcus aureus polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
- 24. A Staphylococcus aureus polypeptide antigen comprising at least one epitope derived from a Staphylococcus aureus polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
- 25. A polypeptide comprising at least one epitope encoded by a Staphylococcus aureus amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
- 26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
- 27. A diagnostic kit for detecting Staphylococcus aureus infection comprising
  - (a) an isolated polypeptide antigen of claim 24, and
  - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
- 28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
- 29. A method of vaccinating an individual against Staphylococcus aureus infection comprising, administering to an individual the vaccine composition of claim 28.



# Figure 2



**DNA Sample Files** 

(Macintosh)

AB 373 and 377

Thousands of Sequences

and Ordering of

[TIGR Assembler]

[asm\_align]